

FIGURE 1

CGCCCGCGCGCGGGCTCAACTTGTAGAGCGAGGGGCCAACTTGGCAGAGCGCGCGGCCA
GCCTTGAGAGAGCGCCCTCCAGGGACTATGCGTGCAGGGACACGGGATCTACCCATACC
ATTGACTAATGGAAGATTATAACAAAATAGAGAAAATTGGAGAAGGTACCTATGGAG
TTGTGTATAAGGGTAGACACAAAATACAGGTCAAGTGGTAGCCATGAAAAAAATCAGAC
TAGAAAGTGAAGAGGAAGGGTCTCTAGTACTGCAATTGGGAAATTCTCTATTAAAGG
AACTCGTCATCCAAATATAGTCAGTCTCAGGATGTGCTTATGCAGGATTCCAGGTTAT
ATCTCATCTTGAGTTCTTCCATGGATCTGAAGAAAATCTTGGATTCTATCCCTCCTG
GTCAGTACATGGATTCTCAGCTGTTACTCAACTCCAGTTGACATTGGAGTATAGGCACCATAT
TATTGCTGGGGTCAGCTGTTACTCAACTCCAGTTGACATTGGAGTATAGGCACCATAT
TTGCTGAACTAGCAACTAAGAAACCACCTTCCATGGGGATTCAAGAAATTGATCAACTCT
TCAGGATTTCAGAGCTTGGGCACTCCCAATAATGAAGTGTGGCCAGAAGTGGAAATCTT
TACAGGACTATAAGAATACATTCCCAATGGAAACCAGGAAGCCTAGCATCCCATGTCA
AAAACCTGGATGAAATGGCTTGGATTGCTCTCGAAAATGTTAATCTATGATCCAGCCA
AACGAATTCTGGCAAAATGGCACTGAATCATCCATATTTAATGATTGGACAATCAGA
TTAAGAAGATGTAGCTTCTGACAAAAAGTTCCATATGTTATGTCAACAGATAGTTGTG
TTTTATTGTTAACTCTGTCTATTTGCTTATATATTTCTTGTATCAAACCTTC
AGCTGTACTTCGTCTCTAATTCAAAAATATAACTTAAAAATGTAATATTCTATATGA
ATTTAAATATAATTCTGTAATGTGAAAAAAAAAAAAAAAAAAAAAA

FIGURE 2

MEDYTKIEKIGEGTYGVVYKGRHKTGQVVAMKKIRLESEEEGVPVSTAIREISLLKELRH
PNIVSLQDVLMQDSRLYLYFEFLSMDLKKYLDsipPGQYMDSSLVKVVTLWYRSPEVLLG
SARYSTPVDIWSIGTIFAELATKPLFHGDSEIDQLFRIFRALGTPNNEVWPEVESLQDY
KNTFPKWKPGSLASHVKNLDENGLLSSKMLIYDPAKRISGKMALNHPYFNDLDNQIKKM

cAMP- and cGMP-dependent protein kinase phosphorylation site.

217-220

Tyrosine kinase phosphorylation site.

9-15

N-myristoylation site.

27-32

43-48

134-139

164-169

190-195

Protein kinase domain
4-230

FIGURE 3A

CCTCGGTTCTATCGATTGAATTCCCCGGGATCCTCTAGAATGGAAAAGTACCACGTGT
GGAGATGATGGAGAAGGCTCTTGGGAGGGTGTACAAGGGTCAAGAAAATACAGTGC
TCAGGTCTGGCCCTGAAGTTCACTCCAAAATTGGGGCGCTCAGAGAAGGAGCTGAGGAA
TTGCAACGAGAGATTGAAATAATGCGGGTCTGCGGCATCCACATTGTGCATATGCT
TGACAGCTTGAAACTGATAAAGAGGTGGTGGTGGTGTACAGACTATGCTGAGGGAGAGCT
CTTCAGATCCTAGAAGATGACGAAAACCTCCTGAAGACCAGGGTCAAGGCATTGCTGC
CCAGTTGGTGTCAAGCCTGTACTATCTGCATTCCACCGCATCACCAGAGATATGAA
GCCTCAGAACATCCTCCTGCCAAGGGTGGTGGCATCAAGCTCTGTGACTTTGGATTG
CCGGGCTATGAGCACCAATAACATGGTGTACATCCATAAAGGCACACCACTCTATAT
GTCTCAGAGCTGGTGGAGGAGCACCATAACGACCACACAGCGGACCTCTGGTCTGTTGG
CTGCATACTATATGAACTGGCAGTAGGCACCCCTCCCTCTATGCTACAAGCATCTTCA
GCTGGTCAGCCTCATTCCTCAAGGACCTGTGCGCTGGCCCTCAACCATCAGTCCCTGCTT
TAAGAACTTCCTGCAGGGACTGCTCACCAAAGACCCACGGCAGCAGTGTCTGGCCAGA
CCTCTTATATCACCCCTTATTGCTGGTCATGTCACCATAATAACTGAGCCAGCAGGCC
AGATTGGGGACCCATTCAACCAGCCCTACCCCCAGAACCTCAGGTCTAAAGGACGA
ACAGGCCATCGGTTGGCCCCAAGGTAATCAGTCTGCATCTGACTCAGGCCTATAA
ACGCATGGCTGAGGAGGCCATGAGAACATCAGAACACAGGACCTGCCCTGAGCA
AGAGGACAAGACCAGCAAGGTGGCTCTGGCACAGCCCTCTGCCAGACTCGGGGCCAC
TCCTCAGGAATCAAGCCTCTGGCCGGACTTAGCCTCAGAATTGAAGAGCAGCTGGGC
TAAATCAGGACTGGAGAGGTGGCTCTGCACCTCGGAAACCCAGGACCCCCAGATG
TGAACGAGCATTCCCGAGAGGAGGCCAGAGGTGCTGGCCAGGGAGCAGTGTAGT
GGACCTGGAAAATGAGGAGGCCAGACAGTGACAATGAGTGGCAGCACCTGCTAGAGACCAC
TGAGCCTGTGCCTATTCAACTGAAGGCTCTCACCTGCTGTAATCCTGACTTCTG
CCAGCGCATCCAGAGTCAGTGCATGAAGCTGGAGGGCAGATCTGAAAGGCATCTGGA
GGGTGCTCCACATCCTGCCATTCGGGCTCTGAGCAGTCTCTCTCAGCTGCAG
TGATTCTGTTGCCTGTATTCCCTCTGCCGGGAGGCAGGGCTCTGGCTGCTGAG
TCTACTCAGGCACAGTCAGGAGAGCAACAGCCTCCAGCAGCAACTTGGTATGGGACCTT
CTTACAGGACCTGATGGCTGTGATTCAAGGCTACTTTGCCTGTAACCTCAACTCTGGAGAG
GAGCCAGACAAGTGACAGCCTGCAGGTGTTAGGAGGCTGCCAACCTTTCTGGACCT
GTTGGGAAACTGCTGCCAACAGAGTGAACACTTGAGCAGACTTGCAGGAGGACAGCT
TATGTGCTTACTGCTCTGTGCAAGCCATGGATGGAAACAGCCGGCCATCTCAAAGC
CTTTTACTCCAGCTGCTGACGACACAGCAGGTTGCTTGGATGGGCTCCTCATGGCTT
GACAGTTCCACAGCTCCCTGTCACACTCCCCAAGGAGCCCGCAAGTGAGCCAGCCACT
GCGAGAGCAGAGTGAGGATACCTGGAGCCATTCCCTGCCCTGGCAGCCATATGCAC
TGCTCCGTGGACTGCCGACTGCTGGATGCCAAGGAGCAGGTGTTGGCATTGG
AAATCAGCTAATGAAAGACAGCAGCCAGCTCAGGCCATCCCTCATCTGCTGCAGCA
TCCCATCCTGTGCCCTGCACCTCTCAAGGTCTATACTCCTGCTGCCCTGTCAGTGAGGG
CCTGTGCCGTCTCTGGGAGCCCTGGCTTGGAAATCCCTGTTATGTTGATTCA
GGCAAGGAAAAGTAGTAGATTGGGAGAGTACTACTGAAGTGACACTCTACTCCCTC
CCTTCTGCTTCTGCCCTAAACCTGCCCTGTTGGAAATGGAGAAGCTAGGCAGTGACGT
TGCTACTCTCTTACCCATTGCGATGTCGCTCTCTTGAGTGAGTCAGCAGCCTGTCATT
GGGACAGCTTGGTCAGCAAGGGGTGACCTTGCACCTCCAGGCCATGGAATGGATGGCTGC
AGCCACACATGCCCTGCTGCCCTGAGAGGTTGGTGAETCCACCAAGGTAGTTG
ATTCTATGATGCCCTCTTATCCTCTGTTGCAGCTCTCACTGAGCAGGGAAAGGCTAG
CTTAATCAGGGATATGTCAGTCAGAAATGTTGGACCGTTTGTGGCACCGCTTCTCCAT
GGTCTGAGGCTCCCCGAGGAGGCATCTGCACAGGAAGGGAGCTTCGCTATCCAGTCC
ACCAAGCCCTGAGCCAGACTGGACACTGATTCTCCCCAGGGCATGGCAGCCCTGCTGAG
CCTGGCCATGCCACCTTACCCAGGAGGCCAGTTATGCCCTGAGCTGCCCTGCTGCCAGCA
TGGAAAGTATCCTCATGTCCTGAGGACTCTGCTCTGGCCCAAGCTTCTGAAATCAACT
GCGCCAGGGCCTCATGGGCTGAGTTCTCCCTGTCGTTGGTGCCTCTGCTGCCAGCT
CCTTGCTCCCCCTGGCAGCATGGATGCTGACCTCCTTATAGTTGCTTGGCCGA
CCTCAGGGACTCAGAAGTTGCAAGCCCCTGCTGCAAGGTCTGCTGCTACCATCTCCGTT
GATGCAAGTGGAGCTGCCCATCAGCCTCTCACACGCCCTGGCCCTCATGGATCCCACCTC
TCTCAACCAGTTGTAACACAGTGCTGCCCTCCCTAGAACCATGTCCTGTTCTCTC
AGTTGCCCTCTGAGTGACCGCCACTGTTGACCTCCGACCTCTCTCTGCTGGCCA
TACTGCCAGGGCTCTGCTCTCCAGCCACTGTCCTTATCCAAGAGCTCTGGCTGGCTC
TGATGAATCCTATGCCCTCTGCCAGCCTCCCTGGCCACCCAGAGAATTGTTGCGGGC
ACACACTTATAGGCTCTGGGACACTTGCTCCAACACAGCATGCCCTGCCCTGGGGCACT
GCAGAGCCAGTCTGGACTGCTCAGCCTCTGCTGCTGCTGGGCTGGAGACAAGGATCCTGT
TGTGCGGGTGCAGTGCAGCTTGTGCTGGGCAATGCAAGCTACCAAGGGCTGGCCTCTGG
ACCTGCCCTGGCAGCTGCAGTGCCCAAGTGAACCCAGCTGCTGGAGATCCTCAGGCTGG
TATCCGGCGCAATGTTGCATCAGCTGGCAACTTGGGACCTGAAGGTTGGGAGAGGA

FIGURE 3B

GCTGTTACAGTGCAGTACCCAGCGGCTCTAGAAATGGCATGTGGAGACCCCCAGCC
AAATGTGAAGGAGGCTGCCCTCATGCCCTCCGGAGCCTGCAACAGGAGCCTGGCATCCA
TCAGGTACTGGTGTCCCTGGGTGCCAGTGAGAAAATACCTTGCTCTCTGGGAATCA
GTCACTGCCACACAGCAGTCCTAGGCCTGCCAACACTGCAGGAAACTCATTCA
CCTCCTGAGGCCAGCCATAGCATGTGAAAGCTTGGCCGCCATGGCCC

FIGURE 4A

MEKYHVLEMIGEGSFGRVYKGRRKYSQQVVALKFIPKLGRSEKELRNLQREIEIMRGLRH
 PNIVHMLDSFETDKEVVVTDYAEGELFQILEDDGKLPEQVQAAQQLVSALYLYLHSRH
 ILHRRDMKPQNILLAKGGGIKLCDFGFARAMSTNTMVLTSIKGTPLYMSPELVEERPYDHT
 ADLWSVGCILYELAVGTPPFYATSIFQLVSLILKDPVRWPSTISPCFKNFLQGLLTKDPR
 QRLSWPDLLYHPFIAGHVTIITEPAGPDLGTPFTSRLPPELQVLKDEQAHRLAPKGNQSR
 ILTQAYKRMAEEAMQKHQNTGPALQEDKTSKVAPGTAPLPRLGATPQESSLLAGILAS
 ELKSSWAKSGTGEVPSAKPRENRTPDCEARFPEERPEVLGQRSTDVVVDLENEEPDSDNEW
 QHLLETTTEPVPIQLKAPLTLNCDFCQRIQLHEAGGQILKGILEGASHILPAFRVLS
 SLLSSCSDSVALYSFCREAGLPGLLSLLRHSQESNSLQQQSWYGTFLQDLMAVIQAYFA
 CTFNLERSQTSDSLQVFQEAANLFLLGGKLLAQPDDEQTLRRDSLMCFTVLCEAMDGN
 SRAISKAFYSSLLTQQVVLGGLTVQPLPVHTPQGAPQVSQPLREQSEDIPGAISS
 ALAAICTAPVGLPDCWDAKEQVCWHLANQLTEDSSQLRPSLISGLQHPILCILHLLKVLYS
 CCLVSEGLCRLLGQEPLAELSFMLIQQGKVVVDWEESTEVTLYFLSLLVFRQLQNLPCGM
 EKLGSDVATLFTSHVVSLSVAAACLLGQLGQGVTFDLQPMEMAAATHALSAPAEVRL
 TPPGSCGFYDGLLLQLLTEQGKASLIRDMSSEMWTVLWHRFSMVLRLPEEASAQEG
 ELSLSSPPSPEDWTLISPQGMAALLSLAMATFTQEPQLCISCLSQHGSILMSILKHL
 PSFLNQLRQAPHGSEFLPVVVLSVCQLLCFFALDMADLLIVVLADLRSEVAHLLQV
 CCYHPLMQLMQUELPISLLTRLALMDPTSLNQFVNTVSASPRТИVSFLSALLSDQPLLTSD
 LLSSLLAHTARVLSPLSHLSFIQEILLAGSDESYRPLRSLLGHPENSVRAHTYRLLGHLLQHS
 MAIRGALQSQSGLLSLLGLGDKDPVVRCASFAGVNAAYQAGPLGPALAAAVPSMTQL
 LGDPQAGIRRNVASALGNLGPEGLGELLOQCEVPQRLLEMACGDPQPNVKEAALIALRSL
 QQEPMIHQVLVSLGASEKLSLLSLGNQSLPHSSPRPASAKHCRKLIHLRPAHSM

N-glycosylation site.

297-300
 381-384
 1286-1289

Glycosaminoglycan attachment site.

369-372

cAMP- and cGMP-dependent protein kinase phosphorylation site.

23-26
 583-586

N-myristoylation site.

138-143
 270-275
 356-361
 400-405
 464-469
 503-508
 599-604
 622-627
 656-661
 671-676
 784-789
 1106-1111
 1145-1150
 1207-1212

Amidation site.

6/46

FIGURE 4B

Leucine zipper pattern.

769-790
987-1008

Serine/Threonine protein kinases active-site signature.

121-133

Protein kinase domain
1-294

FIGURE 5A

CAGAGCGAGGGCGAGAGCCGATCAGCGGATCACCGAGTCTCGCCAGGTGGTGGAGCTGGCA
 GTGAAGGAGCACAAGGCTGAGATTCTGCTCTGCAGCAGGCTCTAAAGAGCAGAAGCTG
 AAGGCCGAGAGCCTCTGACAAGCTCAATGACCTGGAGAAGAAGCATGCTATGCTTGA
 ATGAATGCCCGAAGCTACAGCAGAAGCTGGAGACTGAACGAGAGCTCAAACAGAGGCTT
 CTGGAAGAGCAAGCCAATTACAGCAGCAGATGGACCTGCAGAAAAATCACATTCCGT
 CTGACTCAAGGACTGCAAGAAGCTAGATCGGGCTGATCTACTGAAGACAGAAAGAAGT
 GACTTGGAGTATCAGCTGGAAAACATTCAAGGTTCTTATTCTCATGAAAAGGTGAAAATG
 GAAGGCACTATTCTCAACAAACCAACTCATTGATTCTGCAAGCAAAATGGACCAA
 CCTGCTAAAAAGAAAAGGTTCTCTGCAGTACAATGAGCTGAAGCTGGCCCTGGAGAAG
 GAGAAAGCTCGCTGTGCAGAGCTAGAGGAAGCCCTCAGAAGACCCGCATCGAGCTCCGG
 TCCGCCCGGGAGGAAGCTGCCACCGCAAAGCAACGGACCAACCCACACCCATCCACGCCA
 GCCACCGCGAGGCAGCAGATGCCATGTCGCCATCGCGTCGCCAGAGCACCAGCCC
 AGTCCATGAGCTGTCGCCATCCAGCCGCAAAGGGAGTCTCAACTCCAGAG
 GAATTAGTCGGCTCTTAAAGGAACGCAGCACCAACATTCCTCACCAGATTCAACGTA
 GGACTGAACATGCGAGGCCAAAGTGTGCTGTGATCCGACTTGGAC
 CAGGCATCCAAATGTCGAAATGTCAGGTGATGTGTCACCCCAAGTGTCTCACGTGCTG
 CCAGCCACCTGCGGCTGCCGTGTAATGCCACACACTCACCGAGGCCCTCTGCCGT
 GACAAAATGAACCTCCCAGGTCTCAGACCAAGGAGCCAGCAGCAGCTGCCACCTGGAA
 GGGTGGATGAAGGTGCCAGGAATAACAAACGAGGACAGCAAGGCTGGGACAGGAAGTAC
 ATTGTCCTGGAGGGATCAAAAGTCTCTATTATGACAATGAAGCCAGAGAAAGCTGGACAG
 AGGCCGGTGGAGAATTGAGCTGTGCCCTCCGACGGGGATGTATCTATTATGAGT
 GTTGGTCTCCGAACCTCGAAATACAGCAAAGCAGATGTCCCATACATACTGAAGATG
 GAATCTCACCGCACACCCACTGCTGGCCCGGAGAACCCCTACTTGCTAGCTCCCAGC
 TTCCCTGACAAACAGCGCTGGGTCACCGCCTTAAAGTCAAGTGTGCTGAGGAGTT
 TCTAGGGAAAAGCAGAAGCTGATGCTAAACTGCTTGGAAACTCCCTGCTGAAACTGGAA
 GGTGATGACCGTCTAGACATGAACATGCAACCGCTGCCCTCAAGTGCAGGAGTGTGGT
 GGCACCGAGGAAGGGCTCTACGCCCTGAATGTTGAAACTCCCTAACCAGTCTCCA
 GGAATTGGAGCAGTCTCCAAATTATATTCAAGGACCTGGAGAAGCTACTCATGATA
 GCAGGAGAAGAGCGGGCACTGTGCTTGTGGACGTGAAGAAAGTGAACAGTCCCTGGCC
 CAGTCCCACCTGCCCTGCCAGCCGACATCTCACCCAAACATTTGAAGCTGTCAAGGGC
 TGCCACTTGGGGCAGGCAAGATTGAGAACGGGCTCTGCATCTGTGCAGCCATGCC
 AGCAAAGTCGTCAATTCCGCTACAACGAAACCTCAGCAAATACTGCATCCGAAAGAG
 ATAGAGACCTCAGAGCCCTGCAGCTGTATCCACTTCACCAATTACAGTATCCTCATTGGA
 ACCAATAAAATTCTACGAAATCGACATGAAGCAGTACACGCTCGAGGAATTCTGGATAAG
 ATAGACCATCTTGGCACCTGCTGTTGCGCCTTCCAAACAGCTTCCCTGTCTCA
 ATCGTGGAGGTGAAACAGCGCAGGGCAGCAGAGGAGTACTTGCTGTGTTCCACGAATT
 GGAGTGGTCTGGATTCTACGGAAGACGTAGCCGCACAGACGATCTCAAGTGGAGTC
 TTACCTTGGCCTTGCCTACAGAGAACCCATCTGTTGACCCACTCAACTCACTC
 GAAGTAATTGAGATCCAGGCACGCTCCTCAGCAGGGACCCCTGCCGAGCGTACCTGGAC
 ATCCCGAACCGCGCTACCTGGGCCCTGCCATTCTCAGGAGCGATTACTTGGCGTCC
 TCATACCAGGATAAAATTAAAGGGTCAATTGCTGCAAGGGAAACCTCGTGAAGGAGTC
 ACTGAACACCACCGGGCCCGTCCACCTCCCGCAGCAGCCCAAACAGCGAGGCCACCC
 ACGTACAACGAGCACATACCAAGCGCTGCCCTCCAGCCAGGCCAGGCCAGGCCAGC
 AGCCACCCCGAGAGCCAAGCACACCCACCGCTACCCGGAGGGGGAGCCGAGCTGCC
 AGGGACAAGTCTCTGGCCGCCCTGGAGCAGAGAAGTCCCCGGCGATGCTCAGC
 ACGCCGGAGAGAGCGGTCCCCCGGGAGGCTGTTGAAGACAGCAGCAGGGCCGGCTGCC
 CGGGAGCGGTGAGGACCCCGCTGTCCTCAGGTGAACAAGGTCTGGGACCAAGTCTCAGTA
AAAATCTCAGCCAGAAAACCAACTCCTCATCTGATCTGCAGGAAAACACCAACAC
 TATGGAACCTGCTGATGGGGACCCAAGGCCACGTGCTAGCCACCCCTCTGGCTCAGC
 GGGGCCAGACCCACCTCGGCACGGACACCCCTGTCTCCAGGAGGGCAGGTGGCTGAGG
 CTCTCGGAGCTGTCAGCGCCGGTGCCTGCCCTGGCACCTCCCTGCACTCATCTCTT
 GCACATTGTTACTCTTCAAGCATTACAAACTTTGTACCTAGCTAGCCTGTACCA
 GTTAGTTCATCAAAGGAAACCAACCGGGATGCTAACAAACACATGGTTAGAATCTAAATT
 AGCTACTTTAAGATCCTAGGATTGGTTGGTTTTCTTTTTCTCTTTGTTCTTTC
 CTTTTTTTTTTTTTTAAGACAACAGAAATTCTTAATAGATTGAATAGCGACGTATT
 TCCTGTTGTTAGTCATTAGCTGACCGACCATCATCAGGTCTTGCCACCGAGGCATAGT
 GTAGAACAGTCCCGTCAAGTGGCCAACCTCCCGCAGCCAAGTAGGTTCATCCTTGT
 TGTTCATTCGCTTTATGGCCTTGACGACTCCCTCCACCGCTGAGAATGTATGGA
 GGTCACTGGGGCCTCAGCTGGAGGCAGTGACTGGGGCCAAGGGACCTCGAGACGCTT
 CCTCCCCACCCCCCAGCGTCACTCCCCCAGCCTGCTGTTCCGCTTCCATATAGCTT
 GGCCAGGAAAGCATGCAATAGACTTGCTGGAGCCCAGCACTCCTGGTCTCGGGTC
 CGG

FIGURE 5B

GGAGGGGACGGGGGACCCACTTCTTGTGACGGCGTGTGTTCCCCACTCTGGGA
TGGGGAAAGAGGCCGTGGGAGTTCTGCATGGCAGTTCACTGCATGTGCTGCCCCCTTGG
GTGCTCTGCCAATGTATTAATACCATCCCAGCTCTGCCAAATCGAGACCCCTGTGAC
GACTTGCCGACTAAGCTGGCACCCACAAGCTGCAGTCTGAGCACTGAACAAACAAAAAC
AAAACGCTCAAGCCTAACCTACGACAGAGAAGGATTTCAGCAAACCCACCTCCACTCAGT
GTCCCCCTCCAAACTTCACACTTCCCTGCCTGCAGAGGACTCTGTTCACACCCAAATCC
AGCGCGGTTCTACCCCCACGAAACTGTGACTTTCCAAATGAGCCTTCCCTAGGGCTAGAC
CTAAGACCAAGGAAGTTGAGAAAGCAGCCGAGCTCAACTCTTCAGCTCCGCCAGGGTT
GGGAAGTCCTTAGGTGCAGTGCAGCTCCACTGGGTCTGCAGGACCTCCTATTAGAGTAC
GAAATTCTGGCAACTGGTATAGAACCAACCTAGAGGCTTGCAGTTGGCAAGCTAACCTC
GCAGCCCTTACCTGCCTTAATCTCCCACAAAGGCATCTGTTGCTTGGGTCTCCACGA
CTCTTAGGCCCGCCTCAACAACCCAGGCACCTCTAGTAGGCTAAAGGTAGACCCGTT
TCCACCGCAGCAGGTGAACATGACCGTGTCTCAACTGTGTCACAGTTCAAGATCCCTT
CCAGATTGCAACCTGGCCTGCATCCCAGCTCTCTGCTGTCTTAACCTAACGTGCT
TTCTGTTGAAACGCTACAAACCTCATGTGGTAGCTCTGGCAAATGTCTGCTG
TGGCGTTTATGTGTTGCTTGGAGCTGTGGGGCTGACTCTCCCTCCCGTCCCCAG
GGCAGATTGATTGAATGTTGCTGAAGTTGCTCTGGTCCACAGTATTGGAAAGG
TCACTGAAATGGGTCTTCAGTCTGGCATTTCATTAGGATCTCCATGAGAAATGGGC
TTCTTGAGCCCTGAAAATGTATATTGTGTGTCATCTGTGAACGTCTTGCTATATA
GAACTAGCTCAAAAGACTGTACATATTTACAAGAAACTTTATATTCTGAAAAAAAG
AGGAAATTGAATTGGTTCTACTTTTATTGTAAAAGGTGCATTTCAACACTTACCT
TTGGTTCAATGGTGGTAGTTGTTGGACAGCCATCTCACTGGAGGGTGGGAGCTCCGTG
TGACCACCAAGATGCCAGCAGGATATACCGTAACACGAAATTGCTGTCAAAGCTTATTA
GCATCAATCAAGATTCTAGGTCTCCAAAAGTACAGGCTTTCTCATTACCTTTTAT
TCAGAACGAGGAAGAGAACACAAGGAATGATTCAAGATCCACCTTGAGAGGAATGAACCT
TGTTGTTGAACAATTAGTGAATAAGCAATGATCTAAACT

9/46

FIGURE 6

MLEMNARSLQQKLETERELKQRLLEEQAKLQQQMDLQKNHIFRLTQGLQEALDRADLLKT
ERSDLEYQLENIQVLYSHEKVKMGTISQQTKLIDFLQAKMDQPAKKKKVPLQYNELKLA
LEKEKARCAELEEALQKTRIELRSAREEAAHRKATDHPHPSTPATRQQIAMSIAVRSP
HQPSAMSLIAPPSSRRKESSTPEEFSRRLKERMHNIPIHFRNVGLNMRAVKCAVCLDTVH
FGRQASKCIECQVMCHPKCSTCLPATCGLPAEYATHTEAFCRDKMNSPGLQTKEPSSSL
HLEGWMKVPRNNKRGQQGWDRKYIVLEGSKVLYDNEAREAGQRPVEEFELCLPDGDVSI
HGAVGASELANTAKADVPYIILKME SHPHTTCWPGR TLYLLAPSFPDKQRWVTALESVVA
GRVSREKAEDAKLLGN SLLKLEGDDR LDMN CTL PFS DQVVLVGTEEGLYA
LNVLKNSLT
HVPGIGAVFQIYI I K D L E K L L M I A G E E R A L C L V D V K V K Q S L A Q S H L P A Q P D I S P N I F E A
VKGCHLFGAGK IENG CICAAMP SKV VIL RY N E N L S K Y C I R K E I E T S E P C S C I H F T N Y S I
L I G T N K F Y E I D M K Q Y T L E E F L D K N D H S L A P A V F A A S S N S F P V S I V Q V N S A G Q R E E Y L L C F
H E F G V F V D S Y G R R S T D D L K W S R L P L A F A Y R E P Y L F V T H F N S L E V I E I Q A R S S A G T P A R A
Y L D I P N P R Y L G P A I S S G A I Y L A S S Y Q D K L R V I C C K G N L V K E S G T E H H R G P S T S R S S P N K R
G P P T Y N E H I T K R V A S S P A P P E G P S H P R E P S T P H R Y R E G R T E L R R D K S P G R P L E R E K S P G R
M L S T R R E R S P G R L F E D S S R G R L P A G A V R T P L S Q V N K V W D Q S S V

N-glycosylation site.

451-454
574-577
597-600

cAMP- and cGMP-dependent protein kinase phosphorylation site.

152-155
196-199

N-myristoylation site.

47-52
362-367
420-425
464-469
555-560

Amidation site.

670-673

Carbamoyl-phosphate synthase subdomain signature 2.

1-8

CNH domain
448-745

PH domain
300-419

Phorbol esters/diacylglycerol binding domain
219-267

10/46

FIGURE 7

AAAGGCCTGCAGCAGGACGAGGACCTGAGCCAGGAATGCAGGAATGGCGGCGGTGAAGAAG
 GAAGGGGGTGCCTGTAGTGAAGCCATGTCCCTGGAGGGAGATGAATGGGAACGTAGTAAA
 GAAAATGTACAACCTTAAGGCAAGGGCGGATCATGTCCACGCTTCAGGGAGCACTGGCA
 CAAGAATCTGCCTGTAAACAATACTCTTCAGCAGCAGAAACGGGCAATTGAATATGAAATT
 CGATTTACACTGGAAATGACCCCTCTGGATTTGGGATAGGGTATATCAGCTGGACAGAG
 CAGAACTATCCTCAAGGTGGGAAAGAGAGTAATATGTCAACGTTATTAGAAAAGAGCTGT
 GAAGCACTACAAGGAGAAAAACGATATTATAGTGTACCTCGATTTCATCTGGCTT
 AAATTAGGGCGTTATGCAATGAGCCTTGGATATGTACAGTTACTTGCAACAACCAAGGG
 ATGGTGTTCACTTGCTCAGTTCTATATCTCATGGGAGAAGAAATATGAAGCTAGAGAA
 AACTTAGGAAAGCAGATGCGATATTCAGGAAGGGATCAACAGAAGGCTGAACCACTA
 GAAAGACTACAGTCCCAGCACCAATTCCAAGCTCGAGTGTCTGGCAAACACTGTGTT
 GCACCTGAGAAAGAAGAGGAGAAGTTTGAGTCTCTGTACCCACAAGCAAGCACA
 CTAGCTGAACAAAGAGCAAAGGAAAAGACAGCAAGAGCTCCAAATCATCCGTGAGGA
 GGTGCTCTCAAGGCTCCAAGCCAGAACAGAGGACTCCAAAATCCATTCTCAACAGATG
 CAAAATAATAGTAGAATACTGTTTGATGAAAATGCTGATGAGGCTCTACAGCAGAG
 TTGCTAAAGCTCACAGTCCAGGCCATGGAGACAGCACCCCCATGCCAGGGCAAAGAGAAT
 GAGCTGCAAGCAGGCCATTGGAACACAGGCAGGTCTGGAACACAGGCCCTGTGCAAT
 ACAGCTTCACTGTACAGTGTACCCCTGTCTCCAGTTCACTCCATATGTGGAAGAG
 ACTGCACAACAGCCAGTTATGACACCATGTAAAATTGAACCTAGTATAAACACATCCTA
 AGCACCAGAAAGCCTGGAAAGGAAGAAGGAGATCCTCTACAAAGGGTTCAGAGCCATCAG
 CAAGCGCTGAGGAGAAGAAAGAGATGATGTTGTAAAGGAGAAGATTATGCAAGGA
 GTAGGGAAATTCTCCTTGAAGAAATTGCGGCTGAAGTTTCCGGAAGAAATTAAAAGAG
 CAAAGGGAAAGCCGAGCTATTGACCAAGTGCAAGAGAAGAGAGCAGAAATGCAGAAACAGATT
 GAAGAGATGGAGAAGAAGCTAAAAGAAATCCAAACTACTCAGCAAGAAAGAACAGGTGAT
 CAGCAAGAAGAGACGATGCCATCACAAAGGAGACAACAACTGCAAAATTGCTCCGAGTCT
 CAGAAAATACAGGAATGACTCTATCCAGTTCTGTCAGTAAACTGTTGTGCCAGA
 GAAACTTCACTTGCGGAGAACATTGGCAGGAACAACCTCATTCTAAAGGTCCCAGTGT
 CCTTCTCCATTGGATGAGTTCTTCTTCAGAAAAGAATAAAAGTCTCTGCA
 GATCCCCACGAGTTAGCTCAACGAAGACCCCTGCAAGTTCTCAAAACCTCAGAAAGC
 ATCACCTCAAATGAAGATGTCTCAGATGTTGTGATGAATTACAGGAATTGAACCC
 TTGAGCGAGGATGCCATTACAGGCTTCAGAAATGTAACAATTGTCCTAACCCAGAA
 GACACTTGTGACTTTGCCAGAGCAGCTCGTTGTATCCACTCCTTTCATGAGATAATG
 TCCCTGAAGGATCTCCCTCTGATCCTGAGAGACTGTTACCGGAAGAAGATCTAGATGTA
 AAGACCTCTGAGGACCAGCAGACAGCTGTGCAACTACTACAGTCAGACTCTCAGCATC
 AAGAAGCTGAGCCAAATTGAGACAGCTGTGAAGGCACACACTCCTCTGCTTCTCT
 GGTTCTCTGCCCTCGGTTGCAAGCACCCTCCATCAAATGTCCTCAAATTCTGAGAAA
 CTAGAACTTACTAATGAGACTTCAGAAAACCTACTCAGTCACCATGGTGTACAGTAT
 CGCAGACAGCTACTGAAGTCCCTACCAGAGTTAAGTGCTCTGCAAGAGTTGTGTTAGAA
 GACAGACCAATGCCAAAGTGGAAATTGAGAAGGAATGAAATTAGGTAATGAGGATTAC
 TGCATTAACAGAGAAATACCTAATATGTGAAGATTACAAGTTATCTGGGTGGCGCCAAGA
 AACTCTGCAGAAATTAAACAGTAATAAAAGGTATCTCTCAACCTGTCCCATGGACTTTAT
 ATCAACCTCAAGTTAAAGGAACGTTAAATGAAGATTGATCATTGCAAGCTGTTAT
 CAATATCAAGATGGCTGATTGTTGGCACCAATATAAAACTGCTTCACCCCTCAGGAT
 CTTCTCCAAACACAGTGAATATTACCCATGAAATAACAGTGTGATTATTATAACCTT
 TTGACAATAGTGGAGATGCTACACAAAGCAGAAATAGTCCATGGTACTGAGTCCAAGG
 TGTCTGATTCTCAGAACAGAACATCCACGATCCCTATGATTGTAACAAGAACAAATCAAGCT
 TTGAGAGATAGTGGACTTTCCCTACAGTGTGACCTTAGGGTCAGCTGGATGTTTAC
 CTCAGCGGCTTCGGACTGTACAGATCCTGGAAGGGACAAAAGATCCTGGCTACTGTTCT
 TCTCCCTACCAAGGTAGACCTGTTGGTATAGCAGATTAGCACATTACTATTGTTCAAG
 GAACACCTACAGGTCTCTGGATGGCCTCTGGAAACTTAGCAGAAATTCTGAG
 CTAAAAGATGGTAATTGGAATAAAATTCTTGTGCGGATTCTGAATGCCAATGAG
 GCCACAGTGTCTGTTCTGGGGAGCTGCAAGCAGAAATGAATGGGTTTGACACTACA
 TTCCAAAGTCACCTGAACAAAGCCTTATGGAAGGTAGGAAAGTTAAGTACTAGTCCTGGGCT
 TTGCTCTTCAGTGAGCTAGGCAATCAAGTCTCACAGATTGCTGCTCAGAGCAATGGTT
 GTATTGTGGAACACTGAAACTGTATGTGCTGTAATTAAATTAGGACACATTAGATGCA
 CTACCATGCTGTTCTTGTGACAGGTATTTGACGTACTGATAATTGTTAT
 ACAGTGTATATCTTACTCATGGCCTGTCTAAGTGTGAAAGAAACTATTTATTCTAAA
 CAGACTCATTACAAATGGTACCTGTTATTAAACCCATTGCTCTACTTTCCCTGTA
 CTTTCCCATTTGTAATTGTAATTGTTCTTATGATCACCATGTTATTGTAATAA
 TAAAATAGTATCTGTTAAAAAAAAAAAAAAAAAAAAAA

11/46

FIGURE 8

MAAVKKEGGALSEAMSLEGDEWELSKENVQPLRQGRIMSTLQGALAQESACNNTLQQQKR
 AFYEIRFYTGNDPLDVWDRYISWTEQNYPQGGKESNMSTLLERAVEALQGEKRYSDPR
 FLNLWLKLGRLCNEPLDMYSYLHNQGIGVSLAQFYISWAEEYEARENFRKADAIFQEGIQ
 QKAEPLERLQSQHRQFQARVSROTLLALEKEEEEVFESSVPQRSTLAEKSKGKKTARA
 PIIRVGGALKAPSQNRLQNPFPQQMQNNSRITVFDENADEASTAELSKPTVQPWIAPP
 PRAKENELQAGPWNTGRSLEHRPRGNSTASLIAVPAVLPSFTPYVEETAQQPVMTPCKIEP
 SINHILSTRKGKEEGDPLQRVQSHQASEEKKEKMMYCKEKIYAGVGEFSFEEIRAEVF
 RKKLKEQREAELLTSAEKRAEMQKIEEMEKKLEIQTQQERTGDQQEETMPTKETTKL
 QIASESQKI PGMTLSSSVQVNCARETSLAENIWOEQPHSKGPSVPFSIFDEFLLSEKK
 NKSPPADPPRVLQAORRPLAVLKTSSESITSNEDVSPDVCDEFTGIEPLSEDAAITGFRNVT
 ICPNPEDTCDFAARAARFVSTPFHEIMSLKDLPSDPERLLPEEDLDVKTSEDQQTACGTIY
 SQTLSIKLSPPIEDSREATHSSGFSGSSASVASTSSIKCLQIPEKLELTNETSENPTQS
 PWCSQYRRQLLKSLPELSASAELCIEDRPMPKLEIEKEIELGNEDCYIKREYLICEDYKL
 FWVAPRNSAELTVIKVSSQPVPDFYINLKLKERLNEDFDHFCSCYQYQDGCIIVWHQYIN
 CFTLQDLLQHSEYITTHEITVLIYNNLTIVEMLHKAЕIVHGDLSPRCLILRNRIHDPYDC
 NKNNQALKIVDFSYSVDLRVQLDFTLSGFRTVQILEGQKILANCSSPYQVDLFGIADLA
 HLLLFFKEHLQVFWDGFWKLSQNISELKDGELWNKFFVRILNANDEATVSVLGEAAEMN
 GVFDTTFQSHLNKALWKVGKLTSPGALLFQ

N-glycosylation site.

52-55
 97-100
 268-271
 598-601
 711-714
 944-947
 983-986

cAMP- and cGMP-dependent protein kinase phosphorylation site.

667-670

Tyrosine kinase phosphorylation site.

908-914

N-myristoylation site.

8-13
 92-97
 146-151
 148-153
 325-330
 491-496
 657-662
 687-692
 1021-1026

Amidation site.

233-236

FIGURE 9

GGAAGACTTGGGTCTTGGTCGCAGGTGGGAGCCGACGGGTGGGTAGACCGTGGGGAT
ATCTCAGTGGCGGACGAGGACGGCGGGACAAGGGCGGCTGGTCGGAGTGGCGGAGCGT
CAAGTCCCTGCGTCTCCGCTCCGCTGAGTGTCTGGCGCTGCCTGTGCCCCGCCA
GCGCCTTGACATCCGCTCCTGGGACCGAGGCGCCCTGAGGATACTGCTTGTACTTAT
TACAGCTAGAGGCATCATGGACCGATCTAAAGAAAAGCTCAGGACCTGTTAAGGC
TACAGCTCCAGTTGGAGGTCCAAAAGCTGTTCTCGTGTACAGCAGAAATTCTGTCAGAA
TCCATTACCTGTAATAGTGGCCAGGCTCAGGGCTTGTGTCTTCAAATTCTCCA
GCGCGTCTCTTGCAGCACAAAAGCTTGTCTCCAGTCACAAGCGGTTAGAATCAGAA
GCAGAAGCAATTGCAGGCAACCAGTGTACCTCATCCTGTCCTCCAGGCCACTGAATAACAC
CCAAAAGAGCAAGCAGCCCCGTCATCGGACCTGAAAATAATCTGAGGAGGAACGGC
ATCAAAACAGAAAATGAAGAATCAAAAAGAGGCAGTGGGCTTGGAGACTTGAAT
TGGTCGCCCTCTGGTAAAGGAAAGTTGTAATGTTATTGGCAAGAGAAAAGCAAAG
CAAGTTTATCTGGCTCTTAAAGTGTATTAAAGCTCAGCTGGAGAAAGCGGGAGTGG
GCATCAGCTCAGAAGAGAAGTAGAAATACAGTCCACCTCGGCATCCTAATATTCTTAG
ACTGTATGGTATTTCATGATGCTACCGAGTCTACCTAATTCTGGAATATGCACCACT
TGGAACAGTTATAGAGAACCTCAGAAAATTCAAAGTTGATGAGCAGAGAACTGCTAC
TTATATAACAGAATTGGCAAATGCCCTGCTTACTGTCATTGAGAGAGCTTAAATTGCA
AGACATTAAGCCAGAGAACTTACCTCTGGATCAGCTGGAGAGCTTAAATTGCA
TGGGTGGTCAGTACATGCTCCATCTCCAGGAGGACACTCTGTGGCACCCCTGGACTA
CCTGCCCTGAAATGATTGAAGGTGGATGCATGATGAGAAGGTGGATCTGGAGCCT
TGGAGTTCTTGCTATGAATTTTAGTTGGGAAGCCTCTTGAGGGCAAACACATACCA
AGAGACCTACAAAAGAATATCACGGGTGAATTCACATTCCCTGACTTTGTAACAGAGGG
AGCCAGGGACCTCATTCAGACTGTTGAAGCATAATCCAGCCAGAGGCAATGCTCAG
AGAAGTACTGAAACACCCCTGGATCACAGCAAATTCAAAACATCAAATTGCCAAA
CAAAGAATCAGCTAGCAAACAGTCTAGGAATCGTCAGGGGAGAAATCCTTGAGCCAG
GGCTGCCATATAACCTGACAGGAAACATGCTACTGAAGTTATTACATTGACTGCTGC
CCTCAATCTAGAACGCTACACAAGAAATTGTTACTCAGCAGGTGTGCCTTAACCT
CCCTATTAGAAAGCTCCACATCAATAAACATGACACTGTAAGTAAAGTAGCCACGAG
ATTGTGCTACTTAACTGGTTCATATCTGGAGGCAAGGTTGACTGCAGCCGCCCGT
CAGCCTGTGCTAGGCATGGTGTCTCACAGGAGGCAAATCCAGAGCCTGGCTGTGGGAA
AGTGACCACTCTGCCCTGACCCCGATCAGTTAAGGAGCTGTGCAATAACCTTCCTAGTAC
CTGAGTGAGTGTAACTTATTGGTTGGCGAAGCCTGGTAAAGCTGTTGGAAATGAGTAT
GTGATTCTTTAAGTATGAAAATAAGATATATGTACAGACTTGTATTCTCTGTT
GGCATTCCCTTAGGAATGCTGTGTCTGCCGCACCCCGTAGGCCCTGATTGGGTTTC
TAGTCCTCCCTAACCACTTATCTCCCATATGAGAGTGTGAAAAATAAGGAACACGTGCTCT
ACCTCCATTAGGGATTGCTTGGGATACAGAAGAGGCCATGTGCTCAGAGCTGTTAAG
GGCTTATTCTTAAACATTGGAGTCATAGCATGTGTTAAACTTAAATATGCAAATA
ATAAGTATCTATGTCTAAAAAAAAAAAAAA

FIGURE 10

MDRSKENCISGPVKATAPVGGPKRVLVTQQIPCQNPLPVNSGQAQRVLCPSNSSQRVPLQ
AQKLVSSHKPVQNQKQKQLQATSVPHPVSRPLNNTQSKQPLPSAPENNPEEELASKQKN
EESKKRQWALEDFEIGRPLGKGKFGNVYLAREKQSKFILALKVLFKAGVEHQLRR
EVEIQSHLRHPNIRLRLYGYFHDATRVYLILEYAPLGTVYRELQKLSKFDEQRTATYITEL
ANALSYCHSKRVIHRDIKPENLLGSAGEELKIADFGWSVHAPSSRRTTLCGTLDDYLPPEM
IEGRMHDEKVDLWSLGVLCYEFLVGKPPFEANTYQETYKRISRVEFTPDFVTEGARDLI
SRLLKHNPSQRPMILREVLEHPWITANSSKPSCQNKEASKQS

N-glycosylation site.

52-55
93-96
386-389

cAMP- and cGMP-dependent protein kinase phosphorylation site.

285-288
339-342

Tyrosine kinase phosphorylation site.

326-334

Serine/Threonine protein kinases active-site signature.

252-264

Protein kinase domain
133-383

FIGURE 11

GGCGGGACAGTCCGCCGAGGTGCTCGGTGGAGTCATGGCAGTGCCCTTGTGGAAGACTGGACTTGGTCAAACCCCTGGGAGAAGGTGCCTATGGAGAAGTTCAACTGCTGTGAATAGAGTAACGTGAAAGCAGTCGAGTGAAGATTGTAGATATGAAGCGTGCCTGAGACTGTCAAGAAAATTTAAGAAAGAGATCTGTATCAATAAAATGCTAAATCATGAAAATGTAGTAAATTCTATGGTCACAGGGAGAGAAGGCATATCCAATATTATTCAGGAGTACTGTAGTGGAGGAGAGCTTTTGACAGAAATAGAGCCAGACATAGGCATGCCCTGAGAACCAGATGCTCAGAGATTCTTCCATCAACTCATGGCAGGGGTGGTTATCTGCATGGTATTGAAATACTCACAGGGATATTAAACCAAGAAAATCTTGTGGATGAAAGGGATAACCTCAAAATCTCAGACTTTGGCTTGGCAACAGTATTCGGTATAATAATCGTGAGCGTTGTTGAACAAGATGTGTGGTACTTACCATATGGCTCCAGAACTTCTGAAGAGAAAGAGAATTTCATGCAGAACCAAGTGTGTTGGCCTGTGGAATAGTACTTACTGCAATGCTCGCTGGAGAATTGCCATGGGACCAACCCAGTGCAGCTGAGGAGTATTCTGACTGGAAAGAAAAAAACATACCTCAAACCTTGGAAAAAAATGATTCTGCTCCTCTAGCTCTGCTGCATAAAATCTTAGTTGAGAACTCCATCAGCAAGAAATTACCAATTCCAGACATCAAAAAGATAGATGGTACAACAAACCCCTCAAGAAAGGGCAAAAGGCCGAGTCACTTCAGGTGGTGTGTCAGAGTCTCCAGTGGATTTCAGCACATTCAATCCAAATTGGACTCTCTCAGTAAACAGTGCTCTAGTGAAGAAAATGTGAAAGTACTCCAGTTCTCAGGCCAGAACCCGCACAGGTCTTCCAGGCCACATGTCCTGATCATATGCTTGAATAGTCAGTTACTGGCACCCCCAGGATCCTCACAGAACCCCTGGCAGCGGGTGGTCAAAAGAATGACACGATTCTTACCAAATTGGATGCAGACAAATCTTACATGCCTGAAAGAGACTTGTGAGAAGTTGGCTATCAATGGAAGAAAAGTTGTATAATCAGGTTACTATCAACAACACTGATAGGAGAAACAATAAAACTCATTTCAAAGTGAAATTGGTTAGAAATGGATGATAAAATTTGGTGACTTCCGGCTTCTAAGGGTGTGGATTGGAGTTCAAGAGACACTCCTGAAGAGATTAAGGGAGCTGATTGATATTGTGAGCAGCCAAGGGTTGGCTTCTGCCACATGATCGGACCATCGGCCTGGGAATCCTGGTGAATATAGTCTGCTATGTTGACATTCTCCCTAGAGAAGATATCTGTCTGCCTGCAAACGTGCAAATAGTAGTTCTGAAAGTGTTCCTCCCTGTTATCCAAACATCTCCAATTATTGGTTGGCATAACAATAACCTATCTTAATTGTAAGCAAAACTTGGGAAAGGATGAATAGAATTCAATTGATTATTCCTCATGTTGTTAGTATCTGAATTGAAACTCATCTGGTGGAAACCAAGTTTCAGGGGACATGAGTTCCAGCTTTATACACACGTATCTCATTTTATCAAACATTGGTT

15/46

FIGURE 12

MAVPFVEDWDLVQTLGEGAYGEVQLAVNRVTEEAVAVKIVDMKRAVDCPENIKKEICINK
MLNHENVVKFYGHREGNIQYLFLEYCSGGELFDRIEPDIGMPEPDAQRFFHQLMAGVY
LHGIGITHRDIKPENLLDERDNLKISDFGLATVFRYNNRERLINKMCGTLPYVAPELLK
RREFHAEPVDVWSCGIVLTAMLAGELPWDQPSDSCQEYSDWKEKTYLNPKWKKIDSAPLA
LLHKILVENPSARITIPDIKKDRWYNKPLKKGAKRPRVTSGGVSESPSGFSKHIQSNLDF
SPVNSASSEENVKYSSSQPEPRTGLSLWDTSPSYIDKLVQGISFSQPTCPDHMLLNSQLL
GTPGSSQNFWQRLVKRMTRFFTLDADKSYQCLKETCEKLGYQWKKSCMNQVTISTTDRR
NNKLIFKVNLLEMDDKILVDFRLSKGDGLEFKRHFLKIKGKLIDIVSSQKVWLPAT

cAMP- and cGMP-dependent protein kinase phosphorylation site.

375-378

Tyrosine kinase phosphorylation site.

383-390

394-402

N-myristoylation site.

123-128

195-200

341-346

361-366

Serine/Threonine protein kinases active-site signature.

126-138

Protein kinase domain
9-265

FIGURE 13

CCGC GG TTCCGGCTGCTCCGGCGAGGCGACCCTGGGTCGGCGCTGCGGGCGAGGTGGGC
AGGTAGGTGGCGGACGGCCGGTTCTCCGGCAAGCGCAGGCGGGAGTCCCCCACGG
CGCCCGAAGCGCCCCCGCACCCCGGCTCAGCGTTGAGGCAGGGAGTGAAGGAGATG
CCGACCCAGAGGGACAGCAGCACCATGTCCACACCGGTCGCAAGCGGGGGAGCAGCGGGGAC
CATTCCCACCCAGGTCCGGGTGAAAGCCTACTAACCGCAGGGGATATCATGATAAACACATT
GAACCTCCATCTCCTTGAGGGCCTTGCAATGAGGTTGAGACATGTGTTCTTGAC
AACGAACAGCTCTCACCATGAAAAGGATAGATGAGGAAGGAGACCGTGACAGTATCA
TCTCAGTGGAGTTAGAAGAAGCCTTAGACTTTATGAGCTAAACAAGGATTCTGAAC
TTGATTATGTGTTCCCTTGTGTAACAGCAGTCCTGGGATGCCTGTCCAGGGAGAAGAT
AAATCCATCTACCGTAGAGGTGCAAGCCGCTGGAGAAAGCTTATTGTGCCAATGCCAC
ACTTCCAAGCCAAGCGTTCAACAGGCCTGCTCACTGTGCCATCTGCACAGACCGAATA
TGGGGACTTGGACGCCAAGGATATAAGTCATCAACTGCAAACCTTGGTTCATAGAAG
TGCCATAAAACTCGTCACAATTGAATGTGGGCGGCATTCTTGCCACAGGAACCGAGTG
CCCATGGATCAGTCATCCATGCATTCTGACCATGCACAGACAGTAATTCCATATAATCCT
TCAAGTCATGAGAGTTGGATCAAGTGGTGAAGAAAAAGAGGCAATGAACACCAGGGAA
AGTGGCAAAGCTTCATCCAGTCTAGGTCTCAGGATTTGATTTGCTCCGGGTAATAGGA
AGAGGAAGTTGCAAAGACTGTTGATGAGGATATTGATTGGGTACAGACA
ATGAAAGTTGTGAAAAAAGAGCTTGTAAATGATGAGGATATTGATTGGGTACAGACA
GAGAAGCATGTGTTGAGCAGGCATCCAATCATCCTTCTTGTGGGCTGCATTGTC
TTTCAGACAGAAAGCAGATTGTTCTTGTATAGAGTATGTAATGGAGGAGACCTAATG
TTTCATATGCAGCGACAAAGAAAATTCCTGAAGAACATGCCAGATTTACTCTGCAGAA
ATCAGTCTAGCATTAAATTATCTTCATGAGCGAGGGATAATTATAGAGATTGAAACTG
GACAATGTATTACTGGACTCTGAAGGCCACATTAAACTCACTGACTACGGCATGTGTAAG
GAAGGATTACGCCAGGGAGATAACACAGCAGCTTCTGTTGACTCCTAATTACATTGCT
CCTGAAATTAAAGAGGAGAAGATTGGTTCACTGTTGACTGGTGGGCTCTGGAGTG
CTCATGTTGAGATGATGGCAGGAAGGTCTCCATTGATATTGTTGGGAGCTCGATAAC
CCTGACCAGAACACAGAGGATTATCTCTCCAAAGTTATTGAAAACAAATTGCGATA
CCACGTTCTGTCTGTAAGCTGCAAGTGTCTGAAGAGTTCTTAATAAGGACCT
AAGGAACGATGGGTTGTCATCCTCAAACAGGATTGCTGATATTCAAGGGACACCGTTC
TTCCGAAATGTTGATTGGGATATGATGGAGCAAAACAGGTGGTACCTCCCTTAAACCA
AATATTCTGGGAATTGGTTGGACAATTGATTCTCAGTTACTAATGAACCTGTC
CAGCTCACTCCAGATGACGATGACATTGTGAGGAAGATTGATCAGTCTGAATTGAGGT
TTTGAGTATATCAATCCTTTGATGTCAGAAGAATGTGTCATCCTCATTTTC
AACCATGTATTCTACTCATGTTGCATTTAATGCATGGATAAAACTGCTGCAAGCCTGGA
TACAATTAAACCATTTATTTGCACCTACAAAAAAACACCCAATATCTCTCTGTAG
ACTATATGAATCAATTATTACATCTGTTTACTATGAAAAAAATTAAACTACTAGCT
TCCAGACAATCATGTCAAAATTAGTTGAACTGGTTTCAGTTTAAAGGCCTACAG
ATGAGTAATGAAGTTACCTTTGTTAAAAAAAG

17/46

FIGURE 14

MSHTVAGGGSGDHSHQVRVKAYYRGDIMITHFEPSISFEGLCNEVRDMCSFDNEQLFTMK
WIDEEGDPCTVSSQLELEEAFLYELNKDSLELIHVFCVPERPGMPCPGEDKSIYRRGA
RRWRKLYCANGHTFQAKRDNRAHCAICTDRIWGLGRQGYKCINCKLLVHKKCHKLVTIE
CGRHSLPQEPMQSSMHSDDHAQTVIPYNPSSHESLDQVGEEKEAMNTRESGKASSSL
GLQDFDLLRIGRGSYAKVLLVRLKKTDRYAMKVVKELVNDDDEDIDWVQTEKHVFQEA
SNHPFLVGLHSCFQTESRLFFFVIEYVNGGDLMFHMQRQRKLPPEHARFYSAEISLALNYL
HERGIIYRDLKLDNVILDSEGHIKLTDYGMCKEGLRPDTTSTFCGTPNYIAPEILRGED
YGFSDVWWALGVLMFEMMAGRSPFDIVGSSDNPDQNTEDYLFQVILEKQIRIPRSLSVKA
ASVLKSFLNKPDKERILGCHPQTGFADIQGHFFRNVDWDMMEQKQVVPFFKPNISGEFGL
DNFDSQFTNEPVQLTPDDDIVRKIDQSEFEGFEYINPLLMSAEECV

N-glycosylation site.

533-536

Tyrosine kinase phosphorylation site.

265-271

N-myristoylation site.

7-12
308-313
394-399

Cell attachment sequence.

24-26

Serine/Threonine protein kinases active-site signature.

365-377

Protein kinase domain
245-513

Protein kinase C terminal domain
514-580

Phorbol esters/diacylglycerol binding domain
132-181

Octicosapeptide repeat
56-85

FIGURE 15

GGGGCGGCGGGCGCGAGTTGCTCATACTTGTGACTTGCCTCACAGTGGCATTAGC
TCCACACTGGTAGAACCAACAGGACAGACAAGCATAGAAACATCTAAACATCTCATC
GAGGCATCGAGGTCCATCCAATAAAAATCAGGAGACCCCTGGCTATCATAGACCTTAGTC
TTCGCTGGTATACTCGCTGCTGCAACCAGCGGTTGACTTTTTAAGCCTCTTTTT
CTCTTTTACCACTTCTGGAGCAAATTCAGGTTGCTCTGGATTGTAATTGTAATG
ACCTCAAAACTTTAGCAGTCTCCATCTGACTCAGGTTGCTCTGGCGGTCTCAG
AATCAACATCCACACTCCGTATTATCTGCGTGCATTTGGACAAAGCTCCAACCAGG
ATACGGGAAGAAGAAATGGCTGGTGATCTTCAGCAGGTTCTCATGGAGGAACCTAAT
ACATACCGTCAGAAGCAGGGAGTAGTACTAAATATCAAGAACTGCCTAATTCAAGGACCT
CCACATGATAGGAGGTTACATTCAAGTTATAATAGATGGAAGAGAAATTCCAGAAGG
GAAGGTAGATCAAAGAAGGAAGCAAAATGCCGAGCAAATTAGCTGTTGAGATACTT
AATAAGGAAAAGAAGGAGTTAGTCCTTATTATTGACAACAACGAATTCTCAGAAGGA
TTATCCATGGGAATTACATAGGCCTTATCAATAGAATTGCCAGAAGAAAAGACTAATC
GTAATTATGAACAGTGTGCATCGGGGTGCATGGGCCAGAAGGATTTCATTATAATGC
AAAATGGACAGAAAGAATATAGTATTGGTACAGGTTACTAAACAGGAACCAAACAA
TTGGCGCTAAACTGCATATCTCAGATTATCAGAAGAAACCTCAGTGAAATCTGAC
TACCTGTCCTCTGGTTCTTGCCTACTACGTGTGAGTCCAAAGCAACTCTTAGTGACC
AGCACACACTCGCTTCTGAATCATCTGAAGGTGACTCTCAGCAGATACTCAGAGATA
AATTCTAACAGTGACAGTTAACAGTTCTCGTTGCTTATGAATGGTCTCAGAAATAAT
CAAAGGAAGGCAAAAGATCTTGGCACCCAGATTGACCTCCTGACATGAAAGAAACA
AAGTATACTGTGGACAAGAGGTTGGCATGGATTAAAGAAATAGAATTAAATTGGCTCA
GGTGGATTGGCCAAGTTTCAAAGAAAACACAGAATTGACGGAAAGACTTACGTTATT
AAACGTGTTAAATATAAAACGAGAAGGCAGCGTGAAGTAAAGCATTGGCAAAACTT
GATCATGTAATATTGTCACTACAATGGCTGTTGGATGGATTGATTGATCCTGAG
ACCACTGATGATTCTTGAGAGCAGTGATTGATCCTGAGAACAGCAAAATAGTTCA
AGGTCAAAGACTAAGTGCCTTTCATCCAAATGGAATTCTGTGATAAAGGGACCTTGGAA
CAATGGATTGAAAAAGAAGAGGCAGAAACTAGACAAAGTTGGCTTGGAACTCTT
GAACAAATAACAAAAGGGGTGGATTATATACATTCAAACAAATTATCATAGAGATCTT
AAGCCAAGTAATATATTCTTAGATACAAACAGTAAAGATTGGAGACTTGGACTT
GTAACATCTGAAAAATGATGGAAAGCGAACAAAGGAGTAAGGGAACTTGCAGATACTG
AGCCCAGAACAGATTCTCGCAAGACTATGGAAAGGAAGTGGACCTCTACGCTTGGGG
CTAATTCTGCTGAACTCTTCATGTATGTGACACTGCTTTGAAACATCAAAGTTTTC
ACAGACCTACGGGATGGCATCATCTCAGATATATTGATAAAAAAGAAAAACTCTTCTA
CAGAAATTACTCTCAAAGAAACCTGAGGATCGACCTAACACATCTGAAATACTAAGGACC
TTGACTGTGTTGAAAGAAAAGCCCGAGAAAAATGAACGACACACATGTTAGAGCCCTTCT
GAAAAAGTATCTGCTTCTGATATGCACTTCTTAAATTATCTAAATCTGCTAGGG
ATATCAATAGATATTTACCTTTATTTAATGTTCTTAAATTCTTACTATTTTACT
AATCTTCTGAGAAACAGAAAGGTTTCTCTTTGCTTCAAACATTCTTACATT
TACTTTCTGGCTCATCTTTATTCTTTTTAAAGACAGAGTCTCGCTC
TGTGCCCAGGCTGGAGTGCAATGACACAGTCTGGCTCACTGCAACTCTGCCTTGG
GTTCAAGTGAATTCTCTGCCTCAGCTCCTGAGTAGCTGGATTACAGGCATGTGCCACCC
ACCCAACAACTTTGTGTTTAATAAAGACAGGGTTCACCATGTTGCCAGGCTGG
CTCAAACCTGACCTCAAGTAATCCACCTGCCCTGGCTCCAAAGTGTGGATTACA
GGGATGAGCCACCGCGCCAGCCTCATCTCTTGTCTAAAGATGAAAAACACCCCCCA
AATTCTTTTATACATTAAATGAATCAATCAATTCTTATCTTAAATTCTAC
CGCTTTAGGCCAAAAAAATGTAAGATGTTCTGCCTCACATAGCTTACAAGCCAGCT
GGAGAAATAGGTACTCATTTTTTTAAAGTGTACAGCAACC

FIGURE 16

MAGDLSAGFFMEEILNTYRQKQGVVLKYQELPNSGPPHDRRFTFQVIIDGREFPEGEGRSK
KEAKNAAAKLAVEILNKEKKAVSPLLLTTTNSSEGLSMGNYIGLINRIAQKKRLTVNYEQ
CASGVHGPEGFHYKCKMGQKEYSIGTGSTKQEAQOLAALAYLQILSEETSVKSDYLSSG
SFATTCESQSNSLVTSTLASSESSSEGDFSAUTSEINSNSDSLNSSLLMNGLRNNQRKAK
RSLAPRFDLPDMKETKYTVDKRGMDFKEIELIGSGGFQVFKAKHRIDGKTYVIKRVKY
NNEKAEREVKALAKLDHVNVHYNGCWDGFDYDPETSSDLESSDYDPENSKNSSRSKTK
CLFIQMEFCDKGTLEQWIEKRRGEKLDKVLALELFEQITKGVDYIHSKKLIHRDLKPSNI
FLVDTKQVKIGDFGLVTSKNDGKRTSRKGTLRYMSPEQISSQDYGKEVDLYALGLILAE
LLHVCCTAFETSKFFTDLRDGIISDIFDKKEKTLQKLLSKKPEDRPNTSEILRTLTVWK
KSPEKNERHTC

N-glycosylation site.

91-94
223-226
353-356
528-531

cAMP- and cGMP-dependent protein kinase phosphorylation site.

39-42
112-115

Tyrosine kinase phosphorylation site.

285-293

N-myristoylation site.

95-100
99-104
145-150
180-185
231-236
325-330
434-439
475-480

Amidation site.

442-445

Serine/Threonine protein kinases active-site signature.

410-422

Protein kinase domain
267-538

Double-stranded RNA binding motif

10-75
101-165

FIGURE 17

ATGTCTCGGGAGTCGGATGTTGAGGCTCAGCAGTCTCATGGCAGCAGTGCCTGTTCACAG
CCCCATGGCAGCGTTACCCAGTCCAAGGCTCCTCCTCACAGTCCAGGGCATATCCAGC
TCCTCTACCAAGCACCGATGCCAAACTCCAGCAGTCCCTCCTCACAGTCCAGCTCTGGGACACTG
AGCTCCTTAGAGACAGTGTCCACTCAGGAACACTTCTATTCTATTCCCTGAGGACCAAGAACCT
GAGGACCAAGAACCTGAGGAGCCTACCCCTGCCCCCTGGGCTCGATTATGGGCCCTTCAG
GATGGATTGCCAATCTTGAATGTGTGAATGACAACACTGGTTGGGAGGGACAAAAGC
TGTGAATATTGCTTGATGAACCACTGCTGAAAAGAACAGATAAAATACCGAACATACAGC
AAGAAACACTTCCGGATTTTCAAGGAAAGTGGGTCTAAAAACTCTTACATTGCATACATA
GAAGATCACAGTGGCAATGGAACCTTGTAAATACAGAGCTGTAGGGAAAGGAAACGC
CGTCCTTGAATAACAATTCTGAAATTGCACTGTCACTAACAGAAAATAAGTTTGTCT
TTTTTGATCTGACTGTAGATGATCAGTCTAGTTATCTAAGGCATTAAGAGATGAATAC
ATCATGTCAAAAACCTTGGAAAGTGGTGCCTGTGGAGAGTAAAGCTGGCTTCGAGAGG
AAAACATGTAAGAAAGTAGGCCATAAAAGATCATCAGCAAAAGGAAGTTGCTATTGGTTCA
GCAAGAGAGGGCAGACCCAGCTCAATGTTGAAACAGAAAATAGAAATTGAAAGCTA
AATCATCCTGATCATCATCAAGATTAAAAACTTTTGATGTCAGAAGATTATTATATTGTT
TTGGAATTGATGGAAGGGGGAGAGCTGTTGACAAAGTGGTGGGAATAACCGCCTGAAA
GAAGCTACCTGCAAGCTCTATTACCACTGACTTAAAGCCAGAGAATGTTTACTGTCATCTCAAGAAGAG
GACTGTCTATAAAGATTACTGATTGGCACTCCAAGATTGGGAGAGACCTCTC
ATGAGAACCTTATGGAACCCCCACCTACTTGGCGCTGAAGTTCTGTTCTGTTGGG
ACTGCTGGGTATAACCGTGTGGACTGCTGGAGTTAGGAGTTATTCTTTATCTGC
CTAGTGGGTATCCACCTTCTGTGAGCATAGGACTCAAGTGTCACTGAAGGATCAGATC
ACCAGTGGAAAATACAACCTCATTCTGAAGGTCTGGGAGAAGTCTCAGAGAAAGCTCTG
GACCTTGTCAAGAAGTTGGTAGTGGATCCAAGGCACGTTTACGACAGAAGAAC
TTAAGACACCGTGGCTCAGGATGAAGACATGAAGAGAAAGTTCAAGATCTCTGTCT
GAGGAAAATGAATCCACAGCTCTACCCAGGTTCTAGGCCAGCCTCTACTAGTCGAAAG
CGGCCCGTGAAGGGGAAGCCGAGGGTGCCGAGACCACAAAGCGCCCAGCTGTGTGCT
GCTGTGTTGAAACTCCGTGGTTGAACACGAAAGAAATGTCCTTTCACTCTGCATC
TTCTTTCTTGAGTCGTTTATAGTGGATTTAATTATGGAATAATGGTT

FIGURE 18

MSRESDVEAQSHGSSACSQPHGSVTQSQGSSSQSGISSLSTSTMPNSSQSSHSSGTL
SSLETVSTQELYSIPEDEQEPEDQEPPEPTPAPWARLWALQDGFAVNDNYWFGRDKS
CEYCFDEPLLKRTDKYRTYSKKHFRIFREVGPKNSYIAYIEDHSGNGTFVNTELVGKGKR
RPLNNNSEIALSLSRNKVFVFFDLTVDDQSVYPKALREDEYIMSKTLGSGACGEVKLAFER
KTCKKVAIKIISKRKFAIGSAREADPALNVETEIEILKKLNHPCIIKIKNFFDAEDYYIV
LELMEGGELFDKVVGNKRLKEATCKLYFYQMLLAVQYLHENGIIHRDLKPENVLLSQEE
DCLIKITDFGHSKILGETSLMRTLCGTPTYLAPEVLVSGTAGYNRAVDCWSLGVILEFIC
LSGYPPFSEHRTQVSLKDQITSGKYNFIPPEVVAEVSEKALDLVKKLLVDPKARFTTEEA
LRHPWLQDEDMKRKFQDLLSEENESTALPQVLAQPSTSRRKPREGEAEGAETTKRPAVCA
AVL

N-glycosylation site.

48-51
166-169
185-188
503-506

Glycosaminoglycan attachment site.

164-167

Tyrosine kinase phosphorylation site.

289-297

N-myristoylation site.

14-19
37-42
58-63
167-172
227-232
529-534

Amidation site.

177-180

Serine/Threonine protein kinases active-site signature.

343-355

Protein kinase domain

220-486

FHA domain

113-192

22/46

FIGURE 19

GGCACGAGTAGGGGTGGCGGGTCAGTGCTGCTCGGGGGCTTCTCCATCCAGGTCCCTGGA
GTTCTGGCCCTGGAGCTCCGCACTGGCGCGAACCTGCGTGAGGCAGCGCAGCTCTG
GCGACTGGCCGGCCATGCCCTCCGGGCTGAGGACTATGAAGTGTGTACACCATTGGA
CAGGCTCCTACGGCCGCTGCCAGAAGATCCGGAGGAAGAGTGATGGCAAGATATTAGTT
GGAAAGAACCTGACTATGGCTCCATGACAGAAAGCTGAGAAACAGATGCTTGTGATTGAA
TGAATTGCTCGTGAECTGAAACATCCAAACATCGTCGTTACTATGATCGGATTATG
ACCGGACCAATAACAACTGTACATTGAAATTGTGAAGGGAGGGATCTGGCTA
GTGTAATTACAAAGGGAAACCAAGGAAAGGCAATACTTAGATGAAGAGTTGTTCTCGAG
TGATGACTCAGTTGACTCTGGCCCTGAAGGAATGCCACAGACGAAGTGTGTTGGTCATA
CCGTATTGCATCGGGATCTAAACCAGCCAATGTTCTGGATGGCAAGCAAAACGTCA
AGCTTGGAGACTTGGGCTAGCTAGAATATAACCATGACACGAGTTTGCACAAACAT
TTGTTGGCACACCTTATTACATGTCCTGAACAAATGAATCGCATGTCCTACAATGAGA
AATCAGATATCTGGTATTGGGCTGCTGCTGTATGAGTTATGTCATTAATGCTCCAT
TTACAGCTTTAGCCAGAAAGAACCTGCTGGGAAATCAGAGAAGGCAAATTCAAGGCGAA
TTCCATACCGTTACTCTGATGAATTGAATGAAATTATACAGGAGATGTTAAACTTAAAGG
ATTACCATCGACCTCTGTTGAAGAAATTCTTGAGAGAAAGGGCGACAATTAGGAGAGCAGAAAAT
CGCAGGATTCAGCCCTGTATTGAGTGAGCTGAAACTGAAGGAATTCAAGTACAGGAGC
GAGAGCGAGCTCTCAAAGCAAGAGAAGAAAGATTGGAGCAGAAAGAACAGGAGCTTG
TTCGTGAGAGACTAGCAGAGGACAAACTGGTAGAGCAGAAAATCTGTTGAAGAACTACA
GCTTGCTAAAGGAACGGAAGTTCTGTCCTGGCAAGTAATCCAGAACTTCTTAATCTC
CATCCTCAGTAATTAAAGAACGAAAGTTCAATTCACTGAGCTCACATCTAACTGCAAGGACCTGAAGAAA
GGAGTGAGAATTCTGAGAGCTGAGCTCACATCTAACTGCAAGGACCTGAAGAAA
GGCTTCACGCTGCCAGCTGCGGGCTCAAGGCCCTGTCAGATATTGAGAAAATTACCAAC
TGAAGACAGACAGATCCTGGGCATGGC~~T~~AGCCAGGTAGAGAGACACAGAGCTGTGAC
AGGATGTAATTACCAACCTTAAAGACTGATATTCAATGCTGAGTTGAATACCT
GGCCCCATGAGCCATGCCCTTCTGTATAGTACACATGATATTTCGGAATTGTTTACTG
TTCTCAGCAACTATTGTCACAAATGTCACATTAAATTCTCTTTAAGAAC
ATATTATAAAAAGAATACCTTCTGGTTGGCTTTAATCCTGTTGATGTTACTAGTAG
GAACATGAGATGTGACATTCTAAATCTGGGAGAAAAAATAATTAGGAAAAAAATT
TATGCAAGGAAGAGTAGCACTCACTGAATAGTTAAATGACTGAGTGGTATGCTTACAAT
TGTCACTGCTAGATTAAATTAAAGTCTGAGATTAAATGTTTGAGCTTAGAAAC
CCAGTTAGATGCAATTGGTCATTAATACCATGACATCTGCTTATAAAATTCCATTGC
TCTGTAGTTCAAATCTGTTAGCTTGTGAAAATTCACTGACTGATGTTGATTTCTT
TTTTCTGTTAACAGAATATGAGCTGTCATTTACCTACTTCTTCCACTAA
TAAAAGAATTCTCAGTTA

23/46

FIGURE 20

MPSRAEDYEVLYTIGTGSYGRQCQKIRRKSDGKILVWKELDYGSMTEAEKQMLVSEVNLLR
ELKHPNIVRYYDRIIDRTNTTLYIVMEYCEGGDLASVITKGTKEROYLDEEFVLRVMTQL
TLALKECHRRSDGGHTVLRDLKPANVFLDGKQNVKLGDFGLARILNHDTSAKTFVGT
YYMSPEQMNRMMSYNEKSDIWSLGCLLYELCALMPPFTAQSQKELAGKIREGKFRRIPYRY
SDELNEIIITRMLNLKDYHRPSVEEILENPLIADLVADEQRRNLERRGRQLGEPEKSQDSS
PVLSELKLKEIQLQERERALKAREERLEQKEQELCVRERLAEDKLARAENLLKNYSLLKE
RKFLSLASNPELLNLPSSEVIKKVHFSGESKENIMRSENSESQLTSKSKCKDLKKRLHAA
QLRAQALSDIEKNYQLKSRQILGMR

N-glycosylation site.

79-82
354-357

cAMP- and cGMP-dependent protein kinase phosphorylation site.

26-29

Tyrosine kinase phosphorylation site.

100-107

N-myristoylation site.

91-96

Leucine zipper pattern.

306-327
313-334

Serine/Threonine protein kinases active-site signature.

137-149

Protein kinase domain
8-271

24/46

FIGURE 21

TTGGCGGGCGGAAGCGGCCACAAACCGGCGATCGAAAAGATTCTTAGGAACGCCGTACCA
GCCGCGTCTCTCAGGACAGCAGGCCCTGTCCTCTGTCGGCGCCGCTCAGCCGTGCC
TCCGCCCTCAGGTTCTTTCTAATTCCAATAAACTTCAAGAGGACTATGAAAGATT
ATGATGAACTTCTCAAATATTATGAATTACATGAAACTATTGGGACAGGTGGCTTGCAA
AGGTCAAACCTGCCTGCCATATCCTACTGGAGAGATGGTAGCTATAAAATCATGGATA
AAAACACACTAGGGAGTGATTGCCCGGATCAAAACGGAGATTGAGGCCTGAAGAAC
TGAGACATCAGCATATATGTCAACTTACCATGTGCTAGAGACAGCCAACAAAATATCA
TGGTCTTGAGTACTGCCCTGGAGGGAGAGCTGTTGACTATATAATTCCAGGATGCC
TGTCAAGAGGGAGACCCGGGTTGTCTTCCGTCAAGATAGTATCTGCTGTTGCTTATGTC
ACAGCCAGGGCTATGTCACAGGGACCTCAAGCCAGAAAATTGCTGTTGATGAATATC
ATAAATTAAAGCTGATTGACTTTGGTCTGTGCAAACCCAAGGGTAACAAGGATTACC
ATCTACAGACATGCTGAGGAGCTGGCTTATGCAACGACCTGAGTTAATAACAGGCAAAT
CATATCTGGATCAGAGGACAGATGTTGGAGCATGGCATACTGTTATATGTTCTTATGT
GTGGATTCTACCATTTGATGATAATGTAATGGCTTATACAAGAAGATTATGAGAG
GAAAATATGATGTTCCAAGTGGCTCTCCTCCAGTAGCATTCTGCTTCTCAACAAATGC
TGCAGGTGGACCCAAAGAACGGATTCTATGAAAATCTATTGAACCATCCTGGATCA
TGCAAGATTACAACATACCTGTTGAGTGGCAAAGCAAGAATCCTTTATTCAACCTCGATG
ATGATTGCGTAACAGAACTTTCTGTACATCACAGAAACACAGGAAACAAATGGAGGATT
TAATTTCACGTGGCAGTATGATCACCTCACGGCTACCTATCTCTGCTTAGCCAAGA
AGGCTGGGAAAACCAGTCGTTAAGGCTTCTCTCTGTGGACAAGCCAGTG
CTACCCCATTCACAGACATCAAGTCAAATAATTGGAGTCTGGAAGATGTGACCGCAAGTG
ATAAAAATTATGTGGGGGATTAATAGACTATGATTGGTGTGAAGATGATTATCAACAG
GTGCTGCTACTCCCCAACATCACAGTTACCAAGACTGGACAGAATCAAATGGGGTG
AACTAAATCATTAACCTCCAGCCTTATGCAAGAACCTGCAAATAAAATTAAAGAACAAAG
AAATGTATACTCTTAAGCTGCTGTTAAGAAGACTTATGTTCTGAG
CAAAGACTCCAGTTAATAAGAACAGCATAGAGAGAAACTACTACGCAAATCGTT
ACACTACACCCCTCAAAGCTAGAAACCACTGCGCTGAAAGAAACTCCAATTAAACACAG
TAAATTCAACAGGAACAGACAAGTTAATGACAGGTGTCATTAGCCCTGAGAGGCCTGCC
GCTCAGTGGATTGGATCTCAACCAAGCACATATGGAGGAGACTCCAAAAGAACAGGAG
CCAAAGTGGTGGAGCCTTGAAAGGGGTTGGATAAGGTTACTGTGCTCACAGGA
GCAAAGGAAGGGTCTGCCAGAGACGGGCCAGAAGACTAAAGCTCACTATAATGTGA
CTACAACTAGATTAGTGAATCCAGATCAACTGTTGAATGAAATAATGTCTATTCTCAA
AGAAGCATGTTGACTTTGACAAAGGGTTATACACTGAAGTGTCAAACACAGTCAGATT
TTGGGAAAGTGACAATGCAATTGAATTAGAAGTGTGCCAGCTTCAAAACCGATGTGG
TGGGTATCAGGAGGCAGCGGCTTAAGGGCGATGCCCTGGGTTACAAAAGATTAGTGGAAAG
ACATCCTATCTAGCTGCAAGGTATAATTGATGGATTCTTCCATCCTGCCGGATGAGTGTG
GGTGTGATACAGCCTACATAAGACTGTTATGATCGCTTGATTAAAGTTCAATTGGAA
CTACCAACTTGTCTAAAGAGCTATCTTAAGACCAATATCTCTTGTGTTAAACAAA
GATATTATTTGTGATGAATCTAAATCAAGCCCCTGTCATTGTTACTGTCTTTT
TAATCATGTGGTTTGATATTAATAATTGTTGACTTCTTAGATTCACTCCATATGTG
AATGTAAGCTCTTAACATATGTCTTTGTAATGTGAAATTCTTCTGAAATAAAACCAT
TTGTGAATAT

25/46

FIGURE 22

MKDYDELLKYYELHETIGTGGFAKVKLACHILTGEMVAIKIMDKNTLGSIDLPIKTEIEA
LKNLRHQHICQLYHVLETANKIFMVLEYCPGGELFDYIISQDRLSEEETRVVFRQIVSAV
AYVHSQGYAHRLDKPENLLFDEYHKLKLIDFGLCAKPKGNKDYHLQTCCGSLAYAAPELI
QGKSYLGSEADVWSMGILLYVLMCGFLPFDNNVMALYKKIMRGKYDVPKWLSPSSILL
QQMLQVDPKKRISMKNLLNHPWIMQDYNYPVEWQSKNPFIHLDDDCVTELSVHHRNNRQT
MEDLISLWQYDHLTATYLLLAKKARGKPVRLRLSSFSCGQASATPFTDIKSNNWSLEDV
TASDKNYVAGLIDYDWCEDDLSTGAATPRTSOFKYWTESGVESKSLTPALCRTPANKL
KNKENVYTPKSAVKNEEYFMFPEPKTPVNKNQHKREILTPNRYTTPSKARNQCLKETPI
KIPVNSTGTDKLMTGVISPERCRSVELDLNQAHMEETPKRKGAKVFGSLERGLDKVITV
LTRSKRKGSARDGPRRLKLHYNVTTTRLVNPDQLLNEIMSILPKKHVDFVQKGYTLKCQT
QSDFGKVTMQFELEVVCQLQKPDVVGIRRQLKGDAWVYKRLVEDILSSCKV

N-glycosylation site.

354-357
485-488
562-565

cAMP- and cGMP-dependent protein kinase phosphorylation site.

250-253
546-549

Tyrosine kinase phosphorylation site.

2-10
421-427
630-638

N-myristoylation site.

340-345

Microbodies C-terminal targeting signal.

649-652

Leucine zipper pattern.

165-186

Serine/Threonine protein kinases active-site signature.

128-140

Protein kinase domain
11-263

Kinase associated domain 1
602-651

FIGURE 23

GTCTTTATTCAGTCCCGGATCCGGGGCGCAGGCCAGCTCAGGCCCCAGGGATGGAC
GTCGTGGACCTGACATTTCATAAGAGACCCCGGGACCACTATGACCTGCTACAGCGG
CTGGGTGGCGGACGTATGGGAAGTCTTAAGGCTCGAGACAAGGTGTCAAGGGACCTG
GTGGCACTGAAGATGGTAAGATGGAGCCTGATGATGATGTCTCCACCCCTCAGAAGGAA
ATCCTCATATTGAAAACCTGCCGGACGCCAACATCGTGGCCTACCATGGGAGTTATCTC
TGGTTGCAGAAACTCTGGATCTGCATGGAATTCTGTGGGCTGGTCTCTCAGGACATC
TACCAAGTACAGGCTCCCTGTCAGAGCTCCAGATTAGCTATGTCAGGCCGGAAAGTGC
CAGGGACTGGCCTATTGCACTCACAGAAGAAGATACACAGGGACATCAAGGGAGCTAAC
ATCCTCATCAATGATGCTGGGAGGTCAGATTGGCTGACTTGGCATCTGGCCCAGATT
GGGGCTACACTGCCAGACGCCCTCTCTTCAATTGGACACCCCTACTGGATGGCTCCGGAA
GTGGCAGCTGTGGCCCTGAAGGGAGGATAACATGAGCTGTGACATCTGGTCCCTGGC
ATCACGGCATCGAACCTGGCGAGCTACAGGCCACCGCTTTGATGTGCACCCCTCAGA
GTTCTCTTCCATGCCAACAGACTGGCTACCAGCCTCCCCGACTGAAGGAAAAAGGCAA
TGGTCGGCTGCCTTCCACAATTCTCATCAAAGTCACTCTGACTAAAGGTCCCAGAAACGA
CCCAGGCCACCAAGATGCTCAGTCATCAACTGGTATCCCAGCCTGGCTGAATCGAGGC
CTGATCCTGGATCTTCAAAACTGAAGAAATCCCAGGAAAGGACCCCTCCATTGGGAC
ATTGAGGATGAGGAGCCCAGCTACCCCTGCTATCCCTCGCGGATCAGATCCACCCAC
CGCTCCAGCTCTGGGGATCCCAGATGCAAGACTGCTGTCGGCGCACATGGAGTTCA
AAGCTCCAGGAATGGAGACCAGACCCCCAGCCAACACCGCTGCCCTACAGCCTCTGA
GACCTCAGGAGCAGCAGCCCCAGGAAGCAACTGTCAGAGTCGTGACGATGACTATGA
GACGTGGACATCCCCACCCCTGCAGAGGACACACCTCCTCCACTCCCCCAAGGCCAAG
TTCCGTTCTCCATCAGACGAGGGCTGGGAGCATGGGGATGATGGGCAGCTGAGCCG
GGGGTCTGGCTGGGGTGTGCCAGTGGGCCCCACCAAACAGCCCCGTCCTGGGCTCCC
CCATCCACCAGCAGCCCCCACCTCACCAGGCAACTCAGAACCCCTACTCTGGAACCCACCC
TCCCCGGAGCTTGACAAGCCCCACTTCTGCCCCCAAGAAGGAAAAGATGAAGAGAAAG
GGATGTGCCCTCTCGTAAAGTTCAATGGCTGCCCTCGGATCCACAGCACGGCC
GCCTGGACACATCCCTCACCAAGGACCAAGCAGCACCTGCTCTGGGGCAGAGGAAGGCATC
TTCATCCTGAACCGGAATGACCAAGGAGGCAAGCTGGAAATGCTCTTCTAGCCGGACT
ACGTGGGTGACTCCATCAACACGTTCTCATGTCCTCTCAGGAAAGACCCCCCACCTG
TATTCTCATAGCATCCTGGCTGCTGGAACGGAAAGAGACCAAGAGCAGGAAACCCCCATC
GCTCACATTAGCCCCACCGCTACTGGCAAGGAAGAACATGGTTCCACCAAGATCCAG
GACACCAAGGCTGCCGGGCGTGTGTGGCGAGGGTGCAGCTCTGGGGCCGTC
CTGTGGGGCATTGGAGACGTCGGTGTCTGCTCTGCTTCAAGTGGTACCCAGCCATGAACAAA
TTCTGCTTGTCCGGAGGTGCTGTTCCACTGCCAGCGCCCTCTGCTCGTGTGCGCTG
CTGACCGGGCCAGGCTCTGAGCTGCCGCTGTGTCATGCCGAGGCCCCGGCGCCG
GGGAAGTCGGTGTCTTCCACACGGTGCCTTGGCGCGCTCTGCTGGCTGGCGAG
ATGAGCACCGAGCACAGGGACCCGTGCAGGGTACCCAGGTAGAGGAAGATATGGTATG
GTGTTGATGGATGGCTCTGTGAAGCTGGTGAACCCGGAGGGTCCCCAGTCGGGGACTT
CGCACACCTGAGATCCCCATGACCGAAGCGGTGGAGGGCGTGGCTATGGTTGGAGGTCA
CTTCAGGCCCTCTGGAGCATGGAGTGCAGGGTGTGGGCTTAGGCTGGATCAGCTGCTA
CAGGAGCTGAGAGACCCCTACCCCTACTTCCGTCTGCTTGGCTCCCCCAGGCTGGAGTGC
AGTGGCACGATCTGCCACTGCAACCTCCCTCCAGGTTCAAGCAATTCTCCTGCC
TCAGCCTCCCGAGTAGGGATTACAGGCCTAGTGGTGGAGACACGCCAGTGGATG
ATCCTACTGCTCCAGCAACCTCTACATCCAGGAATGAGTCCCTAGGGGGGTGTCAAGGAA
CTAGTCCTGCACCCCTCCCCATAGACACACTAGTGGTCAATGGCATGTCCTCATCTCC
CAATAAACATGACTTTAGCCTCTGCAAAAAAA

27/46

FIGURE 24

MDVVDPDIFNRDPRDHYDLLQRLGGGTYGEVFKARDKVGDLVALKMVKMEPDDDVSTLQ
KEILILKTCRHANIVAYHGSYWLQKLWICMEFCGAGSLQDIYQVTGSLSELOQISYVCRE
VLOGLAYLHSQKKIHRDIKGANILINDAGEVRLADFGISAQIGATLARRLSFIGTPYWMA
PEVAAVALKGGYNELCDIWLQPLFVHPLRVLFLMTKSGYQPPRLKEK
GKWSAAFHNFIKVTLTKSPKKRPSATKMLSHQLVSQPGLNRLGILLDLKDKNPGKGPSI
GDIEDEEPELPPAIPRRIRSTHRSSSLGIPDADCCRHMFRKLRGMETRPPANTARLQP
PRDLRSSSPRKQLESESSDDYDDVDIPTPAEDTPPPPKPKFRSPSDEGGPSMGDDGQL
SPGVLVRCASGPPPNSPRPGPPSPSTSPHLLTAHSEPSLWNPPSRELDKPPPLPPKKEKMK
RKGCALLVLFNGCPLRIHSTAATHPSTKDQHLLLGAEEGIFILNRNDQEATLEMLFPS
RTTWVYSINNVLMSLSGKTPHLYSHSILGLLERKETRAGNPIAHISPHRLLARKNMVSTK
IQDTKGCRACCVVAEGASSGGPFLCGALETSVVLLQWYQPMNKFLVRQVLFPLPTPLSVF
ALLTGPGSELPAVCIGVSPGRPGKSVLFHTVRFGALSCWLGE
VMVLMGDGSVKLVTPEGSPVRLRTPEIPMTEAVEAVAMVGGQLQAFWKHGVQVWALGSDQ
LLQELRDPTLTFRLLGSPRLECSGTISPHCNLLPGSSNSPASASRVAGITGL

cAMP- and cGMP-dependent protein kinase phosphorylation site.

168-171
261-264
573-576

N-myristylation site.

25-30
163-168
278-283
328-333
517-522
579-584
606-611
615-620
625-630
676-681
694-699
761-766

CNH domain
500-805

Protein kinase domain

17-274

28/46

FIGURE 25

GAATTGGCACGAAGGAGAGTAGCAGTGCCTGGACCCAGCTCCTCCCCTTCTCT
CTAAGGATGGCCAGAAGGAGAACTCCTACCCCTGGCCCTACGCCGACAGACGGCTCCA
TCTGGCCTGAGCACCTGCCAGCGAGTCCCTCCGGAAAGAGCCTGTACCCCATCTGCA
CTTGTCCCTCATGAGCCGCTCCAATGTCCAGCCCACAGCTGCCCTGGCCAGAAGGTGATG
GAGAATAGCAGTGGGACACCCGACATCTAACGCGGCACTTCACAATTGATGACTTTGAG
ATTGGGCGCTCTGGGAAAGGCAAGTTGGAAACGTGTACTGGCTCGGGAGAAGAAA
AGCCATTTCATCGTGGCCTCAAGGTCTCTCAAGTCCCAGATAGAGAAGGAGGGCGTG
GAGCATCAGCTGCGCAGAGAGATCGAAATCCAGGCCACCTGCACCATCCAAACATCCTG
CGTCTCTACAACATTTTATGACCGGAGGAGGATCTTGATTCTAGAGTATGCC
CGCGGGGAGCTCTACAAGGAGCTGCAGAAGAGCTGCACATTGACGAGCAGCGAACAGCC
ACGATCATGGAGGAGTTGGCAGATGCTCTAATGTACTGCCATGGAAAGAAGGTGATTCA
AGAGACATAAAGCCAGAAAATCGCTTCTAGGGCTCAAGGGAGAGCTGAAGATTGCTGAC
TTCGGCTGGTCTGTCATGCGACCTCCCTGAGGAGGAAGACAATGTGTGGCACCCCTGGAC
TACCTGCCCTCAGAGATGATTGAGGGCGCATCGACAATGAGAAGGTGGATCTGTGGTGC
ATTGGAGTGCTTGCATGAGCTGCTGGTGGGAACCCATTGAGAGTGCATCACACAAAC
GAGACCTATCGCCGCATCGTAAGGTGGACCTAAAGTTCCCGCTCTGTGCCAACGGGA
GCCCAAGGACCTCATCTCAAACACTGCTCAGGCATAACCCCTCGGAACGGCTGCCCTGGCC
CAGGTCTCAGCCCACCCCTGGTCCGGGCCAACTCTCGGAGGGTGCCTGCCCTCTGCC
CTTCAATCTGTCGCCTGATGGTCCCTGTCATTCACTCGGGTGCCTGTTGTATGTCTG
TGTATGTATAGGGGAAAGAAGGGATCC

29/46

FIGURE 26

MAQKENSYPWPYGRQTAPSGLSTLPQRVLRKEPVTPSALVLMRSRSNVQPTAAPGQKV
MENSSGTPDILTRHFTIDDFEIGRPLGKGKFGNVYLAREKKSHFIVALKVLFKSQIEKEGV
EHLQLRREIEIQAHLLHHPNILRLYNYFYDRRIYIILEYAPRGELYKELOQSCTFDEQRTATI
MEELADALMYCHGKKVIHRDIKPENLLLGLKGELKIAADFGWSVHATSLRRKTMCGTL
DYLPEPEMIEGRIDNEKVDLWCIGVLCYELLVGNPFESASHNETYRRIVKVDLKFPASVPTGAQ
DLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPPSALQSVA

N-glycosylation site.

60-63
278-281

cAMP- and cGMP-dependent protein kinase phosphorylation site.

229-232

Amidation site.

192-195

Serine/Threonine protein kinases active-site signature.

196-208

Protein kinase domain

77-326

FIGURE 27A

GGAATTCCTTTTTTTTTTGAGATGGAGTTCACTCTGGCCAGGCTGGAGTG
 CAATGGCACAATCTCAGCTTACTGCAACCTCCGCCTCCCGGTTCAAGCGATTCTCCTGC
 CTCAGCCTCTCAAGTAGCTGGGATTACAGGCATGTGCCACCACCCCTGGCTAACTAATT
 CTTTCTATTTAGAGATGGGTTTACCATGTTGGCTAGGCTGGTCTGAACCTCTG
 ACCTCAGGTGATCCACTTGCCTGGCCTCCAAAGTGCCTAGGATTACAGCGTGAAACTG
 TGCCTGGCTGATTCTTTTGTGTTGGATTTGAAACAGGGTCTCCCTGGTCGCC
 AGGCTGGAGTGCAGTGGTGCATCTGGCTACTATAACCTCACCTCCTGGTTCAAGT
 GATCCTCCCACTTACGCTCTGAGTAGCTGTGATTACAGGCATGCACCACACCCGG
 CTAATTCTGTATTAGAGACAGGGTTTACCATGTTGCCAGGCTGTTCTCAAA
 CTCCCTGGACTCAAGGGATCCGCCTGCCTCCACTTCCAAAGTCCGAGATACAGGTGTG
 AGTCACCATGCCTGACCTTATAATTCTTAAGTCATTCTGTGTCATTCTCCTAG
 GGTCTCACAAACAAATCTGCATTAGGGTACAATAATCCTTAACCTCATGATTCAACAA
 AGGAAGATGAAGTATTGATGATTAGAAAGGGAAAGTAGTAAGCCCACGACACTCCT
 GGATGATGATCCTAAATCCAGATACAGTAAAAATGGGTATGGAAAGGTAGAATACAAAA
 TTGGTTAAATTAAATTATCTAAATATCTAAAACATTGGATACATTGTTGATGTGA
 ATGTAAGACTGTACAGACTTCTAGAAAACAGTTGGGTTCCATCTTCATTCCCCAG
 TGCAGTTCTGTAGAAATGGAATCCGAGGATTAAAGTGGCAGAGAATTGACAATTGATT
 CCATAATGAACAAAGTGAGAGACATTTAAAGTTAAAGTAAAGACCTTACTGATG
 AACTAAGCTGAATAAAATTCTGCTGATACTACAGATAACTCGGGAACTGTTAACAAA
 TTATGATGATGGCAACAAACCCAGAGGACTGGTTGAGTTGTCACAAACTAGAGAAAA
 ACAGTGTCCGCTAACGTGATGCTCTTAAATAATTGATTGGTCGTTACAGTCAGCAA
 TGAAAGCGCTTCCCCAGATAAAATGGCCAAAATGAGAGTTGGCTAGAATTCAAGTGA
 GATTGCTGAATTAAAGCTATTCAAGAGCCAGATGATGCACGTGACTACTTCAAAATGG
 CCAGAGCAAACGTCAAGAAATTGCTTTGTCATATATCTTGCACAAATTGAACTGT
 CACAAGGTAAATGTCAAAAAAGTAAACAACTTCTCAAAAAGCTGTAGAACGTGGAGCAG
 TACCACTAGAAATGCTGGAAATTGCCCTGCCAATTAAACCTCAAAAAAGCAGCTGC
 TTTCAGAGGAGGAAAAGAAGAATTATCAGCATCTACGGTATTAAACTGCCAACAAATCAT
 TTCCGGTCACTTGGCATTACAGAATAGGAACACAGTTGTGATTCCAGAGGACAGA
 CTACTAAAGCCAGGTTTATATGGAGAGAACATGCCACCACAAAGATGCAGAAATAGGTT
 ACCGGAATTCTTGAGACAAACTAACAAAACAACTAACAGTCATGCCATTGGAAGAGTCC
 CAGTTAACCTCTAAATAGCCAGATTGTGATGTGAAGACAGATGATTCAAGTTGTCACCTT
 GTTTATGAAAAGACAAACCTCTAGATCAGAATGCCAGATTGGTTGCTGGATCTA
 AACCAAGTGGAAATGATTCTGTCATTAAAGAAATTAAAGTCTGTCAAAATAGTCATT
 TCAAGGAACCTCTGGTGTAGATGAAAAGAGTTCTGAACATTATTACTGATTCAATAA
 CCTCTGAAGAATAAAACGAATCAAGTCTCTAGCTAAATTAGAAGAAACTAAAGAGTATC
 AAGAACCGAGGTTCCAGAGACTAACAGAAACAGTGGCAAGCTAACAGAAAGTCAGAGT
 GTATTAAACCGAAATCTGCTGCATCTCAAAACTAACAGTGGCAGATTCCGGACTAGCCCAGA
 AAGTTAAATACAGAGCAGAAACATACCACTTTGAGCAACCTGTCTTCAGTTCAAAAC
 AGTCACCAACAAATCTAACATCTAAATGGTTGACCCAAATCTATTGTAAGACACCAA
 GCAGCAATAACCTTGGATGATTACATGAGCTTTAGAAGACTCCAGTTGTAAGAATGACT
 TTCCACCTGTTGTCAGTTGTCACACCTTATGCCAACCTGCCTGTTCCAGCAGCAAC
 AGCATCAAATACTGCCACTCCACTCTAAATTACAGGTTTACGATCTTCCAGCAGCAA
 ATGAATGCATTGGTAAAGGAAGAATTATTCCATATAAGCAGATAGGAAGTGGAG
 GTTCAAGCAAGGTATTCAGGTGTTAAATGAAAAGAACAGATAATGCTATAAAATATG
 TGAACTTAGAAGAAGCAGATAACCAAACCTCTGATAGTTACCGAACGAAATAGCTTATT
 TGAATAAAACTACAACAAACAGTGTGATAAGATCATCCGACTTTATGATTGAAATCACGG
 ACCAGTACATCTACATGGTAATGGAGTGTGGAAATATTGATCTTAATAGTTGGCTAAAA
 AGAAAAAAATCCATTGATCCATGGGAACGCAAGAGTTACTGGAAAATATGTTAGAGGAG
 TTCAACACAATCCATTGATGTTACAGTGTGATCTTAAACCGAGCTAACCTTCTGA
 TAGTTGATGGAATGCTAAAGCTAATTGATTGGGATTGCAAACCAAAATGCAACCGAGATA
 CAACAAAGTGTGTTAAAGATTCTCAGGTGGCACAGTTAAATTATGCCACAGAGCAA
 TCAAAGATATGTCTCCCTCAGAGAAATGGGAAATCTAACAGATAAGCCCCAAA
 GTGATGTTGGCTTACGGATGTTTGTACTATATGACTTACGGGAAACACCAATTTC
 AGCAGATAATTAAATCAGATTCTAAATTACATGCCATAATTGATCTTAATCATGAAATTG
 AATTCCCGATATTCCAGAGAAAGATCTCAAGATGTGTTAAAGTGTGTTAAAAGGG
 ACCAAAAACAGAGGATATCCATTCTGAGCTCCTGGCTCATCCATTGTCACAAATTCAA
 CTCATCCAGTTAACCAAATGCCAAGGGAAACCACTGAAGAAATGAAATATGTTCTGGGC
 AACCTGTTGGCTGAAATTCTCTAACTCCATTGAAAGCTGCTAAAACCTTATATGAAC
 ACTATAGTGGTGGTGAAGTCATAATTCTTCATCCTCCAAAGACTTTGAAAAAAAAGGG
 GAAAAAAATGATTGTCAGTTATTGTCATGTCAGATAGGAGGTATAAAATATGTT
 GTTAACTCTGAAATCCCTGTTGAAATCTACATTGAAAGACAACATCACTGTCAGTGT
 ATCAGCAAAAAAAATTCACTGAGATTATCTTAAAGAAAATGTCACAAAGCAACAC

31/46

FIGURE 27A

TTATGGCACTGTATA TATTGTAGACTTGT TTTCTCTGTTTATGCTCTTGTAATCTAC
TTGACATCATTACTCTTGGAAATAGTGGGTGGATAGCAAGTATATTCTAAAAACTTG
TAAATAAAGTTTGTGGCTAAATGA

FIGURE 28

MNKVRDIKNKFKNEDLTDELSNKISADTTDNGTVMQIMMMANNPEDWLSLLLKLEKNS
 VPLSDALLNKLIGRYSQAIIEALPPDKYQGQNESFARIQVRFAELKAIQEPDDARDYFQMAR
 ANCKKFQFVHISFAQFELSQGNVKKSKQLLQKAVERGAVPLEMLEIALRNINLQKKQLLS
 EEEKKNLSASTVLTQESFSGSLGHQNRNNSCDSRGQTTKARFLYGENMPQDAEIGYR
 NSLRQTNKTKQSCPGRVPVNLLNSPDCDVKTDDSVVPCFMKRQTSRSECRDLVPGSKP
 SGNDSCELRNLSVQNSHFKEPLVSDEKSSELIITDSITLKNKTESSLAKLEETKEYQE
 PEVPESNQKQWQAKRKSECINQNPAAASSNHWQIPELARKVNTEQKHTTFEQPVFSVSKQS
 PPISTSKWFDPKSICKTPSSNTLDDYMSCFRTPVVKNDFPACQLSTPYGQpacFQQQQH
 QILATPLQNLQVLASSSANECISVKGRIYSILKQIGSGGSSKVFQVLNEKKQIYAIKYVN
 LEEADNQTLDSYRNEIAYLNKLQHQHSDKIIRLYDYEITDQYIYVMVMECGNIIDLNSWLKKK
 KSIDPWERKSYWKNMLEAVHTIHQHGIVHSDLK PANFLIVDGMLKLIDFGIANQMQPDTT
 SVVKDSQVGTVNMPPEAIKDMSSRENGKS SKISPKSDVWSLGCILYYMTYGKTPFQQ
 IINQISKLHAIIDPNHEIEFPDIPEKDLQDVLKCCLKRDPKQRI SIPELLAHPYVQIOTH
 PVNQMAKGTTEEMKYVLGQLVGLNSPNSILKAAKTLYEHYSGGESHNSSSKTFEKKRGK
 K

N-glycosylation site.

90-93
 186-189
 210-213
 247-250
 303-306
 342-345
 546-549
 827-830

cAMP- and cGMP-dependent protein kinase phosphorylation site.

282-285
 374-377
 599-602

Tyrosine kinase phosphorylation site.

351-358
 787-796

N-myristoylation site.

88-93
 297-302
 302-307
 470-475
 516-521
 626-631
 798-803

Amidation site.

838-841

Serine/Threonine protein kinases active-site signature.

627-639

Protein kinase domain

509-775

FIGURE 29

GAATTCCGGGCCGCGTCGACGATCTTGGAGACGGCGACCCAGGCATCTGGGGAGCCAC
 AGAAGTCGTACTCCCTAAACCTGCTTGCTCCCCCTGTGGATGTAACCCCTAGCTGG
 CATTTCGCATCTCAATTGGCTGTGATGGAGGCCTTGGGATTGAGATGGATGAGCC
 AATGGCTTTCTCCCCAGCGTGACCGGTTTCAGGCTGAAGGCCTTTAAAAAAACGA
 GCAGAATTAAACTTGAGGTGTTAAAAAGATATTGAGAAGCTTATGAAGCTGTAC
 ACAGCTTAGTAATGTGTTAAGATTGAGGACAAAATTGAGAAGGCACCTTCAGCTGT
 TTATTGCCACAGCACAGTTACAAGTAGGACCTGAAGAGAAAATTGCTCTAAACACTT
 GATTCCAACAAGTCATCCTATAAGAATTGAGCTGAACCTCAGTGCCTAACAGTGGCTGG
 GGGGCAAGATAATGTCATGGAGTTAAATACTGCTTTAGGAAGAATGATCATGTAGTTAT
 TGCTATGCCATATCTGGAGCATGAGTCGTTGGACATTCTGAATTCTCTTCA
 AGAAGTACGGAAATATGCTTAATCTGTTAAAGCTTGAACAGCATTCATCAGTTGG
 TATTGTTACCGTGATGTTAAAGCCAGCAATTTTTATATAATTAGGCCCTGAAAAAGTA
 TGCTTGGTAGACTTGGTTGGCCCAAGGAACCCATGATACGAAAATAGAGCTTCTAA
 ATTTGTCCAGTCTGAAGCTCAGCAGGAAAGGTGTCACAAAACAAATCCCACATAATCAC
 AGGAAACAAAGATTCCACTGAGTGGCCAGTACCTAAGGAGCTGGATCAGCAGTCCAC
 AAAAGCTCTGTTAAAGACCCACACAAATGCACAAATTCAGATTAACAGAAAAGA
 CGGAAAGGAGGGATCTGAGGCCCTCTGTCCAGCGCTCTGTTTGGAGAAAGAAAATT
 CAATATACACAGCTCCATTTCACATGAGAGCCCTGAGTAAACTCATGAAGCAGTC
 GACTGTGGATGTACTGCTAGAAAGTTAGCAACAAAAAGAAGGCTATTCTACGAAAGT
 TATGAATAGTGCTGTGAGGAAAAGTGCAGTTCTGCCAGCTAGCCTGACCTGTGA
 CTGCTATGCAACAGAAAGTTGTAGTTGCCTTCAAGGCCCTGAGCAGGTTGCC
 TAGGGCAGGTACACCGATTAGAGCACAGAGGCTTGACAAAGTGGCCCAATCAAAC
 TACAGCAATTGACATGTGGCTGAGGTGTCATATTCTTCTTGCTTAGTGGACGATA
 TCCATTATAAAGCAAGTGATGATTAACTGCTTGGCCAAATTATGACAATTAGGG
 ATCCAGAGAAACTATCCAAGCTGCTAAACATTGGAAATCAATATTATGAGCAAAGA
 AGTTCCAGCACAAGACTTGAGAAAACTCTGTGAGGAGACTCAGGGTATGGATTCTAGCAC
 TCCCAAGTTACAAGTGATATACAAGGGCATGCTCTCATCAACCAGCTATTTCAGAGAA
 GACTGACCATAAAGCTTCTGCCCTGTTCAAACACCTCCAGGACAATACTCAGGGAAATT
 ATTAAAAAGGGGGATAGTAATAGCTGTGAGCATTGTTGATGAGTATAATACCAATT
 AGAAGGCTGGAATGAGGTACCTGATGAAGCTTATGACCTGCTTGATAAACTCTAGATCT
 AAATCCAGCTTCAAGAATAACAGCAGAAAGCTTGTGCACTCCATTTTAAAGATAT
 GAGCTTGTGATAATTGATCTCATTTAATGTTACTGTTAGAGGCTAGGATAATAATT
 TACTTTGTAATAGCCACAAGTTGTGTTAGAGCAGAGCAGGATTAAATAATT
 AACATTAGTGTTGGCAGATTCTAAATATAGATTAAGAATAACTTAAATGCTG
 GGATAGTTCTGGGACTAACACATGATCTTCTTGAGTTAACCTACCTAAGTAGATT
 TAGGTGGGTTCTATTAGGTAGATTCTGCTTCTCTTAATTACCTTCACTGACATACA
 GAAAAAGGAGCAGTTAGTTAATTAAATTAAACAGATGTGATGAGGATTAAAT
 GAATCAAAGACTTAATTGAGATTCTTCTAGAGTTATGAGCTAGGTATAGTTGGGAA
 AACTCAACTGGTGTGGCTCTAACATTGTAATAAGAAGATAATTCTTCTT
 CTAGAGGTACATATTAGGCCCTTATGAAACACTAAACAAATGAGGAAATGTTGGTCATGG
 GGCAAAAGTATCACTTAAATTGAAATTGATCCATTCTTAAACACTCTCATGAAAGCATT
 CTGGTGTGAAATTGCCATTCTCTCGGAAATTACATGGTGTGACCACAAAGTTCTGGATGTTTA
 TAAATATTGACGGTTACAGTTGGAAATTAAATAACACACTGGTTGATAAAA
 GGGAGCTGCAGGACCAAGGTGAAGATTGATAGTCAAATGCTTTCTTTGAGTTGT
 ATATTCTACACCATCTTAGATATAATTAGGTAGCTGCTGAAAGGAAAAGTGAATACA
 GAATTGACGGTATTATTGGAGATTCTCTGCGTAGAGCCATCCAGATCTGTATCC
 TGTTTGACTAAGTCTTAGGTGGTTGGGAAGACAGATAATGAAGTAGGCAAAGGAGAAA
 GGACCCAAGGATAGAGGTTATATTGAGAATGGTATATCAATGACAGCATATCAA
 ACTCCTATGGAAAAAGTCTGGTGGTCAGCTGACAGATTCCCTATTAGTAGTCAG
 AATACAGAAATAGTTAGGGACATGTATTCTATTGTTATTGAGCATTGATAGGT
 CAGTATCTACCTAATCTGTTGGTAAGTATAGGATATAAAACCAATTACCAATTGATCTGTC
 TTATGCCATAATCTTAAAAAAATTGAATGCTCTGAATTGATATTCAATAAAAGTTA
 TCCTTTATAAAAAAAAGTCGACGCCCGC

FIGURE 30

MEASLGIQMDEPMAFSPQRDRFQAEGSLKKNEQNFKLAGVKKDIEKLYEAVPQLSNVFKI
EDKIGEGTFSSVYLAQQLQVGPEEKIALKHLIPTSHPIRIAELQCLTVAGGQDNVMGV
KYCFRKNDHVVIAAMPYLEHESFLDILNSLSFQEVREYMLNLFKALKRIHQFGIVHRDVKP
SNFLYNRRKKYALVDFGLAQGTHDTKIELLKFKVQSEAQQERCSONKSHITGNKIPLSG
PVPKELDQQSTTKASVKRPYTNAQIQIKQGKDGKEGSVGLSVQRSVFGERNFNIHSSISH
ESPAVKLMKQSKTVDVLSRKLATKKKAISTKVMNSAVMRKTASSCPASLTCDCYATDKVC
SICLSSRRQQVAPRAGTPGFRAPEVLTKCPNQTTAIDMWSAGVIFLSLLSGRYPFYKASDD
LTALAQIMTIRGSRETIQAAKTFGKSILCSKEVPAQDLRKLCERLRGMDSTPKLTSQI
GHASHQPAISEKTDHKASCLVQTGGQYSGNSFKKGDSNSCEHCFDEYNTNLEGWNEVPD
EAYDLLDKLLDLNPASRITAEALLHPFFKDMSL

N-glycosylation site.

226-229
390-393

Tyrosine kinase phosphorylation site.

41-48

N-myristoylation site.

67-72
112-117
119-124
198-203
202-207
432-437
467-472
506-511

ATP/GTP-binding site motif A (P-loop).

439-446

Serine/Threonine protein kinases active-site signature.

173-185

Protein kinase domain

58-569

FIGURE 31

CCGAGTTACGAGTCGGC~~AAAGCGGCGGGAAAGTT~~CGTACTGGGCAGAACCGCAGCGACGGGTCT
GCGGCTTAGGTGAAAATGCCTCGTGTAAAGCAGCTCAAGCTGGAAGACAGAGCTCTGCA
AAGAGACATCTTGCAGAACATTGCAAGTGGAGAGATAATAACTGACATGGCAAAAAG
GAATGGAAAGTAGGATTACCCATTGCCAAGGAGGCTTGGCTGTATATATCTTGTGAT
ATGAATTCTCAGAGTCAGTTGCCAGTGATGCACCTTGTGTTGAAAGTGGAACCCAGT
GACAATGGACCTCTTTACTGAATTAAAGTTCTACCAACGAGCTGCAAAACCAGAGCAA
ATTCAAGAAATGGATTGTACCCGTAAGCTGAAGTACCTGGGTGTCCTAAGTATTGGGG
TCTGGTCTACATGACAAAAATGGAAAAGTTACAGGTTATGATAATGGATCGCTTGGG
AGTGACCTCAGAAAATATGAAGC~~AAATGCCAAAAGGTTTCTCG~~GGAAA~~ACTGTCTG~~
CAGCTAACGTTAAGAATTCTGGATATTCTGGAAATATATTACAGAGCATGAGTATGTGCAT
GGAGATATCAAGGCCAAATCTTCTGAACTACAAGAACATCTGACCAGGTGACTTG
GTAGATTATGCCCTGCTTATCGGTACTGCCAGAAGGAGTTCAAAAGAACATCAAAGAA
GACCCAAAAGATGTACGATGCCACTATTGAATTACGAGCATCGATGCACACAATGGT
GTGGCCCCATCAAGACGTGGTGAATTGAAATACTGGTTATTGCATGATCCAATGGCTT
ACTGCCATCTCCTTGGAGGATAATTGAAAGATCCTAAATATGTTAGAGATTCCAAA
ATTAGATA~~CAGAGAAAATATTGCAAGTTGATGGACAAATGTT~~CCTGAGAAAAACAAA
CCAGGTGAAATTGCCAAATACATGGAAACAGTGAATTACTAGACTACACTGAAAAACCT
CTTATGAAAATTACGTGACATTCTTGTGCAAGGACTAAAGCTATAGGAAGTAAGGAT
GATGGCAAATTGGACCTCAGTGTGTGGAGAATGGAGGTTGAAAGC~~AAAACAATAACA~~
AAGAAGCGAAAGAAAGAAATTGAAGAACAGCAAGGAAC~~CTGGTGTGAAGATACGGAATGG~~
TCAACACACAGACAGAGGAGGCCATACAGACCCGTTCAAGAACAGAACAGAGTCCAG
AAGTAATTCAGATGCTGAA~~CCAGATT~~TCCTTTCTTGTGACTTTCT
CCTTTCTGTTAGAACTGTTTATTTCCTGTGAGTCTGCGAGGTGGAATTAAATGATTA
AATACTCATGTGTTAGAAAACATAAAACTTTTTATAAAAATATTGTACAATTCAATT
AAAGGCTAATTATGAAATTGAAAATCTCAGGTTAATCTCCTAAGTTATCCC~~AAAGC~~
CGTGTGTTGTGATGTTGGAGTACATATATGAAAATTATTATGACACGCAC~~TTTC~~
TAATCATTGACATTCTCAGAGTGGATAAAAATGTTGACAAAGTCCTCACTTTAAGG
AAATGCAAAGCTAA~~AAACTCTCTTGTGAGTGCAG~~

36/46

FIGURE 32

MPRVKAAQAGRQSSAKRHLAEQFAVGEIITDMAKKEWKVGLPIQGGFGCILADMNSSE
SVGSDAPCVVKVEPSDNGPLFTELKFYQRAAKPEQIOKWIRTRKLKYLGVPKYWGSGLHD
KNGKSYRFMIMDRFGSDLQKIYEANAKRFSRKTVLQLSLRILDILEYIHEHEYVHGDIKA
SNLLNYKNPDQVYLVDYGLAYRYCPEGVHKEYKEDPKRCHDGTIEFTSIDAHNGVAPSR
RGDLEILGYCMIQWLTGHLWPEDNLKDPKYVRDSKIRYRENIASLMDKCFPEKNKPGEIA
KYMETVKLLDYTEKPLYENLRDILLQGLKAIGSKDDGKLDLSVENGGLAKTTKKRKK
EIEESKEPGVEDTEWSNTQTEEAIQTRSRTRKRVQK

N-glycosylation site.

57-60

cAMP- and cGMP-dependent protein kinase phosphorylation site.

147-150

Tyrosine kinase phosphorylation site.

160-167
188-194
241-249
295-302

N-myristoylation site.

40-45
46-51
235-240
347-352
369-374

Cell attachment sequence.

241-243

Serine/Threonine protein kinases active-site signature.

173-185

Protein kinase domain
37-325

FIGURE 33

AGTTGGCGGGAATGGCTGCTCGGGAGGGCAGTGTACCGGGGGCGCTGTAGGCTGTCC
 AGCGATGGATCCCACCGCGGGAAAGCAAGAAGGAGCCTGGAGGGAGGCCGCGACTGAGGA
 GGGCGTGAATAGGATCGCAGTGCCAAAGCCGCCCTCATTGAGGAATTCAAGCATAGTGAA
 GCCCATTAGCCGGGGCGCCTTCGGGAAAGTGTATCTGGGGAGAAAGCCGAAATGTGA
 TGCAAGTAAAGGTTGTTAAAAAAGCAGACATGATCAACAAAATATGACTCATCAGGTCCA
 AGCTGAGAGAGATGCACTGGCACTAAGCAAAAGCCATTCAATTGTCCATTGTATTATTC
 ACTGCAGTCTGCAAACAATGTCTACTTGGTAATGGAATATCTATTGGGGAGATGTCAA
 GTCTCTCCTACATATATATGGTTATTTGATGAAGAGATGGCTGTGAAATATATTTCTGA
 AGTAGCACTGGCTCTAGACTACCTTCACAGACATGGAATCATCCACAGGGACTTGAAACC
 GGACAATATGCTTATTTCTAATGAGGGTCATATTAAACTGACGGATTTGGCCTTCAAA
 AGTTACTTGAATAGAGATATTAAATATGATGGATATCCTTACAACACCATCAATGGCAA
 ACCTAGACAAGATTATCAGAAGACCCAGGACAAGTGTATCGCTTATCAGCTCGTGGG
 ATTTAACACACAAATGCAAGAAAAAAATCAAGACCCCTGCAAACATCCTTCAGCCTGTCT
 GTCTGAACATCACAGCTTCTCAAGGACTCGTATGCCCTATGCTGTAGATCAAAGGA
 CACTACGCCCTATTCTAGCAAATTACTAAATCATGCTTGTGAAACAGTTGCCTCCAACCC
 AGGAATGCCGTGAAGTGTCTAATTCTAATTACTCCAGTCTAGGAAAAGGCTGGCAC
 ATCCAGTGCAGTAGTCATACCCACACCTTCATATCCAGTGTGGAATCAGAATGCCACAG
 CAGTCCCAAATGGAAAAAGATTGCCAGGAAAGTGTGATGAAGCATTGGGCCAACAAATGAT
 GAGTTGGAAATGCAAGTTGAAAGTTATGCGCAAATCTGCAAATGCCATTGAGACGAAAGG
 TTTCATAAAAGGATCTGGAGTTAGCTTTCTCCATTCAACAGCAGTGCCTTCC
 CACCACTGGACGCTTGTGTAACCTTGCTAAAAATGCTCTGGAGTTCTG
 GGAAGCAGTAGAACTGGATGTAATAATATAATGGACACTGACACAAGTCAGTAGG
 TTCCATCAGTCAAATCAGTGGGCTGTGGATTCTGGTGGGATATCTGAAGAGCACCCTGG
 GAAAAAGAAGTTAAAAAGAATTGAGTTGACTCCAGTCTGTGAAAGGTT
 ACAGAATAAAACTGTGTAGAGTATAAGCATAACGAAATGCAAATTGTTATACAAA
 TCAAAATACAGGCTTAACAGTGAAGTGCAGGACCTTAAGCTACAGTCACAAAGTC
 ACAAAATGACTGTGCTAATAAGGAGAACATTGCAATTCTTTACTGATAAACAAAC
 ACCAGAAAAATTACCTATACCAATGATAGCAAAACCTTATGTTGACTCGATGAAGA
 CTGTGAAAAGAATAGTAAGAGGGACTACTTAAGTTCTAGTTTCTATGTTGATGATGA
 TAGAGCTTCTAAAAATTCTATGAACTCTGATTCATCTTCTGGAAATTCTATAAT
 GGAAAGTCCATTAGAAAAGTCAGCCCTTAGATTGAGATAGAACGATTAAGAACCTCTT
 TGAAGAATCAAATATTGAAAGATCCACTTATGTAACACCAGATTGCAAAGAAAAGACCTC
 ACCAAAAGGTGCGAGAACCTGCTGTACAAGAGAGTAACCAAAATGTTAGGTCCCTCC
 TTGGAGGTGCTGAAAACGTTAGCCTCTAAAGAAATGCTGTTCTCGAAGTTAA
 CAGTCATATTAGTCATCCAATTACTCAGAACCATCCAGAACATGACTTCTTTAGA
 TGCAATGGATATTGGCTGCTACAGTGGTTCATATCCCATGGCTATAACCCCTACTCA
 AAAAAGAAGATCCTGTATGCCACATCAGACCCCAAATCAGATCAAGTGGAACTCCATA
 CCGAACTCCGAAGAGTGTGAGAAGAGGGGTGGCCCCGTTGATGATGGCGAATTCTAGG
 AACCCCAAGACTACCTGACCTGAGCTTACTAGGCAGGGCCATGGCTCTGCGGTAGA
 CTGGTGGGCACTTGGAGTTGCTTGAATTCTAACAGGAATTCCCCCTTCAATGA
 TGAAACACCAACAAGTATTCTCAGAATATTCTGAAAGAGATATCCCTGGCCAGAAGG
 TGAAGAAAAGTTATCTGATAATGCTCAAAGTGCAGTAGAAATACTTTAACCAATTGATGA
 TACAAAGAGAGCTGAAATGAAAGAGCTAAACGTCATCCCTCTTCACTGAGTGTGGACTG
 GGAAAATCTGAGCATCAGACTATGCCATTCACTCCCCCAGCCAGATGATGAAACAGATAC
 CTCCTATTGAAACAGGAATACTGCTCAGCACCTGACCGTATCTGGATTAGTCTGTA
GCACAAAAATTCTTCTTCTAGTCTAGCCTCGTGTATAGAATGAAACTTGCATAATTATAT
 ACTCCTTAATAACTAGATTGATCTAAGGGGGAAAGATCATTATTAAACCTAGTTCAATGTG
 CTTTAATGTACGTTACAGCTTCACAGAGTTAAAGGCTGAAAGGAATATAGTCAGTAA
 TTTATCTTAACCTCAAAACTGTATATAATCTTCAAAGCTTTTCATCTATTATTTG
 TTTATTGCACTTATGAAAGCATCAATAAAATTAGAGGACACTATTGAGAGTGA
 GCCACTAGCTGATTCTTCTTCTGATTTCAGTTCACTGTTCACTGTTAGCATTAAA
 ATAATAAAATAATCATACTAGTTCC

FIGURE 34

MDPTAGSKKEPGGAAATEEGVNRIAVPKPPSIEEFSIVKPISRGAFGKVYLQKGGKLYA
 VKVVKKADMINKNMTHQVQAERDALALSKSPFIVHLYYSLQSANNVYLVMEYLIGGDVKS
 LLHIYGYFDEEMAVKYISEVALALDYLHRGIIHRDLKPDNMLISNEGHIKLTDGFLSKV
 TLNRDINMMDILTPPSMAKPRQDYSRTPGQVLSLISLGFNTPIAEKNQDPANILSACLS
 ETSQLSQGLVCPMSVDQKDTTPYSSKLLKSCLETVASNPGMVKCLTSNLLQSRKRLATS
 SASSQSHTFISSVESECHSSPKWEKDCQESDEALGPMMWSWNAVEKLCAKSANAIETKGF
 NKKDLELALSPHIHNSSALPTTGRSCVNLAKKCFSGEVSWEAVELDVNNINMDTDTSQLGF
 HQSNQWAVDGGISEEHLGKRSLSKRNFEVDSSPCKIIQNKKTCEYKHNEMTNCYTNQ
 NTGLTVEVQDLKLSVHKSQQNDANCENIVNSFTDKQQTPEKLPPIPMAKNLMCELDED
 EKNSKRDYLSSSFLCSDDDRASKNISMNSDSSFPGISIMESPQESQPLDSRSIKESSFE
 ESNIEDPLIVTPDCQEKTPKGVENPAVQESNQKMLGPPLLEVLTASKRNAVAFRSFNS
 HINASNNSEPSRMNMTSLDAMDISRAYSGSYPMAITPTQKRRSCMPHQTNPQIKSGTPYR
 TPKSVRGVAPVDDGRILGTPDYLAPELLGRAHGPADVWALGVCLFEFLTGIPPFNDE
 TPQQVFQNLKRDI PWPEGEEEKLSDNAQSAVEILLTIDDTKRAMGKELKRHPLFSDVDWE
 NLQHQTMPFIPQPDDETDSYFETRNTAQHLTVSGFSL

N-glycosylation site.

73-76
 374-377
 564-567
 663-666
 666-669
 674 -677

cAMP- and cGMP-dependent protein kinase phosphorylation site.

700-703

N-myristoylation site.

12-17
 13-18
 52-57
 209-214

Amidation site.

438-441

Serine/Threonine protein kinases active-site signature.

152-164

Protein kinase domain

35-834

FIGURE 35

CAAGAGCCCTTCCTGCAGGGAACCTCAGGCTTCAGAGAGCCAAAAAGTTGGGAGGCCTAA
CCACTTACAGGCCGAAGTGTCCGGGTGGACGCATTGGTAGCCGAAGAAGTCCOAGG
ATTGCCGAAGAAGTCCCAGGATTCCGAAGCGAGCCGAAGCATTGGGACAGTTTCAGAG
ACAGCTGATCGGTTGGAGCTGTGCGCCGAGCAGTCATGGCGGGCCAGAGCTACTACG
CCGGCCGATGGCGAGGGAGCCGCCCGAGGCTGAGGCTCTGGCGAGCCGGAAACGG
AGCAGCCGCTTCTTGAGCGGCCTGGAGCTGGTGAAGCAGGGTGGCGAGGCCGCGTGTTC
CGTGGCCGCTTCCAGGGCCGCGCGCGGTGATCAAGCACCGCTCCCCAAGGGCTACCGG
CACCCGGCGCTGGAGGCAGCGGCTTGGCAGACGGCGACGGTGCAGGAGGCCGGCGCTC
CTCCGCTGCGCCGCTGGAATATCTGCCCAAGGTCTCTCCAACTTAGCCAAGACAATTGGCAG
AACTGCTTATATATGGAAGAAATTGAAGGCTCAGTGAATGTTGAGATTATATTCAAGTCC
ACTATGGAGACTGAAAAAAACTCCCCAGGGTCTCTCCAACTTAGCCAAGACAATTGGCAG
GTTTTGGCTCGAATGCACGATGAAGACCTCATTGATGGTGCATCACCACCTCCAACATG
CTCCTGAAACCCCCCTGGAACAGCTGAACATTGTGCTCATAGACTTGGGCTGAGTTTC
ATTTCAGCACTTCCAGAGGATAAGGGAGTAGACCTCTATGTCCTGGAGAAGGCCTTCCTC
AGTACCCATCCCAACACTGAAACTGTGTTGAAGCCTTCTGAAGAGACTACTCCACCTCC
TCCAAAAGGCCAGGCCAGTGCTAAAAAAATTAGATGAAGTGCCTGAGAGGAAGAAAG
AGGTCCATGGTTGGGTAGAAGAATGTGTATGACAACCACACAGTGAAGCTTTTTC
AAAGTAAATTGAGAAGAAATGCTACAAGTATGAGATGAGATCTAAGTAAAGGTGTTAAGAT
ATTAaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

FIGURE 36

MAAARATT PADGEE PAPEAE ALAAARERSSRFLSGLELVKQGAEARVFRGRFQGRAAVIK
HRFPKGYRHPALEARLGRRTVQEARALLRCRRAGISAPVVFFVDYASNCLYMEIEGSV
TVRDYIQSTMETEKT PQGLSNLAKTIGQVLARMHDEDLIHGDLTTSNMLKKPLEQLNIV
LIDFGLSFISALPEDKGVDLYVLEKAFLSTHPNTETVFEAFLKSYSTSSKKARPVLKKLD
EVRLRGRKRSMVG

cAMP- and cGMP-dependent protein kinase phosphorylation site.

78-81
247-250

N-myristoylation site.

147-152

Amidation site.

76-79
245-248

Tyrosine protein kinases specific active-site signature.

158-170

Protein kinase domain

33-252

FIGURE 37

AGCGCGCGACTTTTGAAAGCCAGGAGGGTTCGAATTGCAACGGCAGCTGCCGGCGTAT
GTGTTGGTCTAGAGGCAGCTGCAGGGTCTCGCTGGGGCGCTCGGGACCAATTGAA
GAGGTACTTGGCCACGACTTATTTCACCTCCGACCTTCCTCCAGGCGGTGAGACTCT
GGACTGAGAGTGGCTTCACAATGGAAGGGATCAGTAATTCAAGACACCAAGCAAATTA
TCAGAAAAAAAGAAATCTGTATTATGTTCAACTCCAACATATAAATATCCGGCCTCTCG
TTTATGCAGAAGCTGGCTTGGTACTGGGTAATGTGACCTAATGAAAAGATCTCCA
AGAGGTTTGTCTCATTCCTGGGCTGTAAAAAAGATTAATCCTATATGTAATGATCAT
TATCGAAGTGTGATCAAAGAGACTAATGGATGAAGCTAAGATTGAAAAGCCTTCAT
CATCCAAACATTGTTGGTTATCGTCTTACTGAAGCCAATGATGGCAGTCTGTGTCCT
GCTATGGAATATGGAGGTGAAAGTCTAAATGACTTAATAGAAGAACGATAAAAGCC
AGCCAAGATCCTTCCAGCAGCCATAATTAAAGTTGCTTGAATATGGCAAGAGGG
TTAAAGTATCTGCACCAAGAAAAGAAACTGCTTCATGGAGACATAAAGTCTCAAATGTT
GTAATTAAAGCGATTGAAACAATTAAATCTGTGATGTAGGAGTCTCTACCAACTG
GATGAAAATATGACTGTGACTGACCCCTGAGGCTTGTACATTGGCACAGGCCATGGAAA
CCCAAAGAAGCTGTGGAGGAGAATGGTGTATTACTGACAAGGCAGACATATTGCTT
GGCTTACTTGTGGAAATGATGACTTTATCGATTCCACACATTAATCTTCAAATGAT
GATGATGATGAAGATAAAACTTTGATGAAAGTGAATTGATGATGAAGCATACTATGCA
GCGTTGGGAACCTAGGCCACCTATTAAATATGGAAGAACTGGATGAATCATAACAGAAAGTA
ATTGAACCTCTCTGTATGCACTAATGAAGACCCCTAAAGATGTCCTCTGCTGCACAC
ATTGTTGAAGCTCTGGAAACAGATGTCTAGTGTACATCTCAGCTGAAGTGTGGCTTGCGT
AAATAACTGTTATTCCAAAATTTACATAGTTACTATCAGTAGTTATTAGACTCTAA
ATTGGCATATTGAGGACCATAGTTCTGTTAACATATGGATAACTATTCTAATATGA
AAATGCTTATATTGCTATAAGCACTTGGAAATTGTACTGGGTTCTGTAAAGTTTAG
AAACTAGCTACATAAGTACTTTGATACTGCTCATGCTGACTTAAACACTAGCAGTAAA
CGCTGTAAACTGTAACATTAAATTGAATGACCATTACTTTATTAAATGATCTTCTTAA
TATTCTATATTAAATGGATCTACTGACATTGACTTGTACAGTACAAAATAAGCT
ACATTGTTAAAACACTGAACCTTTGCTGATGTGTTATCAAATGATAACTGGAAGCT
GAGGAGAATATGCCTCAAAAAGAGTAGCTCTGGATACTTCAGACTCTGGTTACAGATT
GTCTTGATCTGGATCTCCTCAGATCTTGGTTTGCTTTAATTAAATGTATT
TTCCATACTGAGTTAAAATTAAATTGTAACCTTAAGCATTCCCAGCTGTGTA
ACAATAAAACTCAAATAGGATGATAAGAATAAAGGACACTTGGTACCAAGAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 38

MEGISNFKTPSKLSEKKKSVLCASTPTINIPASPFMVKLGFGTGVNVYLMKRSRGLSHSP
WAVKKINPICNDHYRSVYQKRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGE
KSLNDLIEERYKASQDPFPAAIILKVALNMRGLKYLHQEKLLLHGDIKSSNVVIKGDFE
TIKICDVGVSPLDENMTVTDPEACYIGTEPWKPKEAVEENGVI TDKADIFAFGLTLWEM
MTLSIPHINLSNDDDEDKTFDESDFDDEAYYAALGTRPPINMEEELDESYQKVIELFSVC
TNEDPKDRPSAAHIVEALETDV

N-glycosylation site.

196-199
249-252

cAMP- and cGMP-dependent protein kinase phosphorylation site.

16-19

N-myristoylation site.

41-46
118-123

Serine/Threonine protein kinases active-site signature.

163-175

Protein kinase domain
32-320

FIGURE 39

GTGCGATCCGGGCCCCGAGGGCATTAGACGGCGGCTGATTAGCTCCGGTTGCATCACCC
GGACCGGGGGATTAGCTCCGGTTGCATCACCCGGACC GGCGGGCCGGCGCGCACGAGAC
TCGGCAGCGGAAGTGGAGGCGCTCCGCGCGTCCGCTGCTAGGACCCGGCAGGGCTGG
AGCTGGGCTGGGATCCCAGCTGGCAGCAGCGCAGCGGGCCGGCCACCTGCTGGTGC
CTGGAGGCCTCTGAGCCCCGGCGCCGGCCACCGGAAACGACGGGGCGAGATCGGA
GCCACCCCTCTAGCTGCTCCTGCGGGTCCCTGTCCAGGAAGAAGCGGTTGGAGTTGGAT
GACAACCTAGATAACCGAGCGTCCCGTCCAGAAACGAGCTCGAAGTGGGCCCCAGCCCAGA
CTGCCCCCTGCCTGTTGCCCTGAGGCCACCTACTGCTCCAGATCGTGCACACTGCTGTG
GCCACTGCCTCCCGTCTGGGCCCTATGTCCTCCTGGAGGCCGAGGGCGGGCGGCC
TACCAAGGCCCTGCACTGCCCTACAGGCAGTGAGTATACTGCAAGGTGACCCCGTCCAG
GAAGCCCCGGCGTGGAGGCCCTATGCGCGCTGCCCGACAAGCATGTGGCTCGG
CCCACTGAGGTCTGCTGGTACCCAGCTCCTTACCGCTTTCACTCGGACCCATGGG
GACATGCACAGCCTGGTGCAGGCCACCGTATCCCTGAGCCTGAGGCTGCCGTGCTC
TTCCGCCAGATGGCCACCGCCCTGGCGACTGTCACCAAGCAGCTGGTCTGCCGTGAT
CTCAAGCTGTGCTGCTTGTCTCGTGTACGGCCAGATGATCCCTGTTGGACAAGCACCGTGC
CTGGAGGACTCTGCGTGTACTGGCCAGATGATCCCTGTTGGACAAGCACCGTGC
CCAGCCTACGTGGGACCTGAGATACTCAGCTCACGGCCTCATACTCGGGCAAGGCAGCC
GATGTCGGAGCCTGGCGTGGCGCTTCACCATGCTGGCGGCCACTACCCCTCCAG
GACTCGGAGCCTGCTCTGCTTCGGCAAGATCCGCCGGGGCTACGCCTTGCGCTGCA
GGCCTCTCGGCCCTGCCCCGTGCTGGTGTGCTGCCCTTCGTCGGGAGCCAGCTGAA
CGGCTCACAGCCACAGGCATCCCTGCACCCCTGGCTGCGACAGGACCCGATGCCCTTA
GCCCAACCCGATCCCATCTCTGGAGGCTGCCAGGTGGTCCCTGATGGTCTGGGCTG
GACGAAGCAGGGAAAGAGGAGGAGACAGAGAAGTGGTTCTGTATGGCTAGGACCC
ACTACACGCTCAGCTGCCAACAGTGGATTGAGTTGGGGTAGCTCCAAGCCTCTCCTG
CCTCTGAACCTGAGCCAAACCTTCAGTCAGCTTCCAGAAGGGAGAAAGGCAGAACGCTGT
GGAGTGTGCTGTGTCACATCTGCTTGTCCACACATGCAAGTCCCTGCTGGGTGCT
TATCAGGTGCCAAGCCTGTTCTGGTGTGGAGTACAGCAGTGAGCAAGGAGACAAT
ATTCCCTGCTCACAGAGATGACAAACTGGCATCCTGAGCTGACAACACTTTCCATGAC
CATAGGTCACTGTCTACACTGGGTACACTTGTACCAAGTGTGCCCTCCACTGATGCTGG
TGCTCAGGCACCTCTGCTCAAGACAATCCCTTCACAAACAAACCAGCTGCCCTTGAT
CTTGTACCTTTCAAGAGAAAGGGAGGTATCCCTGTCGCCAAAGGCTCCAGGCCCTCTCC
GCAACTCAGGACCCAAGCCCAGCTCACTGTTCCAGCAGTCTGTCCCTGCTC
TTGATTAAGAGATTCTCCTCCAGGCATAAGCCTGGGATTGGCCAGAGATAAGAATCC
AAACTATGAGGCTAGTTCTGTCTAACTCAAGACTGTTCTGGATAGGGTCCAGGCC
TCAACCATGGGCTTCTGACCTGAGCACCAAGGTTGAGGGACAGGATTAGGCAGGGCTG
TCCCTGTCGGCACCTGAAAGTCCCAGGTGGGACTCTCTGGGGACACTTGGGGTCCACAA
TCCCAGGTCCTACTCTAGGTTGGATACCATGAGTATGTATGTTACCTGTGCCCTAAT
AAAGGAGAATTATGAAATAAAAAAAAAAAAAAA

FIGURE 40

MRATPLAAPAGSLSRKKRLEDDNLDTERPVQKRARSGPQPRILPPCLLPLSPPTAPDRAT
AVATASRLGPYVLLPEEGGRAYQALHCPTGTEYTCVYPVQEAPAVLEPYARLPPHKHV
ARPTEVLAGTQLLYAFFTRTHGDMHSLVRSRHRRIPEPEAAVLFRQMATALAHCHQHGLVL
RDLKLCRFVFADRKRLVLENLEDSCVLTGPDDSLWDKHACPAYVGPEILSSRASYSGK
AADVWSLGVALFTMLAGHYPFQDSEPVLLFGKIRRGAYALPAGLSAPARCLVRCLLRREP
AERLTATGILLHPWLQRQDPMPLAPTRSHLWEAAQVVPDGLGLDEAREEEGDREVVLYG

N-myristoylation site.

91-96
341-346

Protein kinase domain

71-315

FIGURE 41

GAAGTTTCTCACTAGGGTCTTCTGGCCCAGCCTTGACTGAAGCTGGCTGGAGACAG
GGGCATTAGAGAAGTGACTCATAGATGGCCTAAAGAAGCAGGGCCACTCAAGGACCCAGG
ACAGAGGGAAGAGGGCCAACCCAGCTGGACCACAGGCAAACCCCATTGCCCTTGAGAGAA
AGAAGAGGAGCCGGTGAAACATGCTGCTGCTGAAGAAACACACGGAGGACATCAGCAGCG
TCTACGAGATCCGCGAGAGGCTCGGCTCGGGTGCCTCTCCGAGGTGGTCTGGCCAGG
AGCAGGGCTCCGACACCTCGTGGCCCTCAAGTGCATCCCCAAGAAGGCCCTCCGGGGCA
AGGAGGCCCTGGTGGAGAACGAGATCGCAGTGCTCCGTAGGATCAGTCACCCAAACATCG
TCGCTCTGGAGGATGTCCACGAGAGCCCTCCACCTTACCTGGCCATGGAACCTGGTGA
CGGGTGGCGAGCTTTGACCGCATCATGGAGCGCGCTCCTACACAGAGAAGGATGCCA
GCCATCTGGTGGGTCAAGGTCTGGCGCGTCTCCTACCTGCACACGCCCTGGGATCGTGC
ACCGGGACACTCAAGCCGAAACCTCCTGTATGCCACGCCCTTGAGGACTCGAAGATCA
TGGTCTCTGACTTTGGACTCTAAAATCCAGGCTGGGAACATGCTAGGCACCGCCTGTG
GGACCCCTGGATATGTGGCCCCAGAGCTTGGAGCAGAAACCTACGGGAAGGCCGTAG
ATGTGTGGCCCTGGCGTCATCTCCTACATCCTGCTGTGGTACCCCCCTTCTACG
ACGAGAGCGACCCCTGAGCTCTCAGCCAGATCCTGAGGCCAGCTATGAGTTGACTXTC
CTTCTGGATGACATCTCAGAATCAGGCAAAGACTTATTGGCACCTCTGGAGCGAG
ACCTTCAGAAGAGGTTCACCTGCCAACAGGCCTTGCGGGACCTTGGATCTTGGACA
CAGGCTTGGCAGGGACATCTTAGGGTTTCAGTGAGCAGATCCGGAAAGAACTTGTCTT
GGACACACTGGAAGCGAGCCTCAATGCCACCTTGTCTGCCACATCCGGAAAGCTGG
GGCAGATCCCAGAGGGCGAGGGGCCCTGAGCAGGGCATGGSCCGXCACAGCCACTXAG
GCCTTCGTGCTGGCCAGCCCCCAAGTGGTGATGCCCAGGXAGATGCCGAGGCCAAGTGG
AXTGAXCCCCAGATTXCTTXC

46/46

FIGURE 42

MLLLKKHTEDISSVYEIRERLGSGAFSEVVLAQERGSAHLVALKCIPKKALRGKEALVEN
EIAVLRRISHPNIVALEDVHESPSHLYLAMELVGGELFDRIMERGSYTEKDASHLVGQV
LGAVSYLHSLGIVHRDLKPENLLYATPFEDSKIMVSDFGLSKIQAGNMLGTACGTPGYVA
PELLEQKPYGKAVDVWALGVISYILLCGYPPFYDESDPELFSQILRASYEFDXPFWDDIS
ESGKDFIRHLLERDLQKRFTCQQALRDLWIWDTGFGRDILGFVSEQIRKNFAWTHWKRA
FNATLFLRHIRKLGQIPEGEGASEQGMXRSHXGLRAGQPPKW

N-glycosylation site.

302-305

cAMP- and cGMP-dependent protein kinase phosphorylation site.

5-8
66-69
257-260

Tyrosine kinase phosphorylation site.

101-108

N-myristoylation site.

118-123
166-171
170-175
334-339

Serine/Threonine protein kinases active-site signature.

132-144

Protein kinase domain

15-270